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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 2402
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Oncofetal Fibronectin variant 7
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank NM 054034
; DATABASE ENTRY DATE: 2005-06-10
US-11-193-561-26

Alignment Scores:
Pred. No.: 8.29 Length: 2402
Score: 54.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 17 Gaps: 0

US-09-581-651D-41 (1-10) x US-11-193-561-26 (1-2402)

Qy 1 ValSerIleProProArgAsnLeuGlyTyr 10
|||||
Db 2208 GTGAGTATCCACCCAGAAACCTTGGATAC 2237

RESULT 2
US-11-193-771-26
; Sequence 26, Application US/11193771
; Publication No. US20060024722A1
; GENERAL INFORMATION:
; APPLICANT: Fisher-Colbrie, Mark
; APPLICANT: Hickok, Durlin
; APPLICANT: LaPointe, Jerome P.
; TITLE OF INVENTION: Samples for Detection of Oncofetal Fibronectin and uses thereof
; FILE REFERENCE: 17101-027001/828
; CURRENT APPLICATION NUMBER: US/11/193,771
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 2402
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Oncofetal Fibronectin variant 7
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: US/11/193,771
; DATABASE ENTRY DATE: 2005-06-10
US-11-193-771-26

Alignment Scores:
Pred. No.: 8.29 Length: 2402
Score: 54.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 17 Gaps: 0

US-09-581-651D-41 (1-10) x US-11-193-771-26 (1-2402)

Qy 1 ValSerIleProProArgAsnLeuGlyTyr 10
|||||
Db 2208 GTGAGTATCCACCCAGAAACCTTGGATAC 2237

RESULT 3
US-11-193-789-26
; Sequence 26, Application US/11193789
; Publication No. US20060024723A1
; GENERAL INFORMATION:
; APPLICANT: Husa, Robert
; APPLICANT: Fisher-Colbrie, Mark
; APPLICANT: LaPointe, Jerome
; APPLICANT: Senyei, Andrew
; APPLICANT: Shorter, Simon
; TITLE OF INVENTION: Methods for detecting Oncofetal Fibronectin
; FILE REFERENCE: 17101-029001/830
; CURRENT APPLICATION NUMBER: US/11/193,789
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 2402
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Oncofetal Fibronectin variant 7
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank NM 054034
; DATABASE ENTRY DATE: 2005-06-10
US-11-193-789-26

Alignment Scores:
Pred. No.: 8.29 Length: 2402
Score: 54.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 17 Gaps: 0

US-09-581-651D-41 (1-10) x US-11-193-789-26 (1-2402)

Qy 1 ValSerIleProProArgAsnLeuGlyTyr 10
|||||
Db 2208 GTGAGTATCCACCCAGAAACCTTGGATAC 2237

RESULT 4
US-11-193-806-26
; Sequence 26, Application US/11193806
; Publication No. US20060024724A1
; GENERAL INFORMATION:
; APPLICANT: Husa, Robert
; APPLICANT: Fisher-Colbrie, Mark
; APPLICANT: LaPointe, Jerome
; APPLICANT: Shorter, Simon
; TITLE OF INVENTION: Oncofetal Fibronectin as a Marker for Health and Disease
; FILE REFERENCE: 17101-028001/829
; CURRENT APPLICATION NUMBER: US/11/193,806
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 2402
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Oncofetal Fibronectin variant 7
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank NM 054034
; DATABASE ENTRY DATE: 2005-06-10
US-11-193-561-26

Alignment Scores:
Pred. No.: 8.29 Length: 2402
Score: 54.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 17 Gaps: 0

US-09-581-651D-41 (1-10) x US-11-193-561-26 (1-2402)

Qy 1 ValSerIleProProArgAsnLeuGlyTyr 10
|||||
Db 2208 GTGAGTATCCACCCAGAAACCTTGGATAC 2237

RESULT 2
US-11-193-771-26
; Sequence 26, Application US/11193771
; Publication No. US20060024722A1
; GENERAL INFORMATION:
; APPLICANT: Fisher-Colbrie, Mark
; APPLICANT: Hickok, Durlin
; APPLICANT: LaPointe, Jerome P.
; TITLE OF INVENTION: Samples for Detection of Oncofetal Fibronectin and uses thereof
; FILE REFERENCE: 17101-027001/828
; CURRENT APPLICATION NUMBER: US/11/193,771
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
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; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 2402
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Oncofetal Fibronectin variant 7
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank NM 054034
; DATABASE ENTRY DATE: 2005-06-10
US-11-193-771-26

Alignment Scores:
Pred. No.: 8.29 Length: 2402
Score: 54.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 17 Gaps: 0

US-09-581-651D-41 (1-10) x US-11-193-771-26 (1-2402)

Qy 1 ValSerIleProProArgAsnLeuGlyTyr 10
|||||
Db 2208 GTGAGTATCCACCCAGAAACCTTGGATAC 2237

RESULT 3
US-11-193-789-26
; Sequence 26, Application US/11193789
; Publication No. US20060024723A1
; GENERAL INFORMATION:
; APPLICANT: Husa, Robert
; APPLICANT: Fisher-Colbrie, Mark
; APPLICANT: LaPointe, Jerome
; APPLICANT: Senyei, Andrew
; APPLICANT: Shorter, Simon
; TITLE OF INVENTION: Methods for detecting Oncofetal Fibronectin
; FILE REFERENCE: 17101-029001/830
; CURRENT APPLICATION NUMBER: US/11/193,789
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 2402
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Oncofetal Fibronectin variant 7
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank NM 054034
; DATABASE ENTRY DATE: 2005-06-10
US-11-193-789-26

Alignment Scores:
Pred. No.: 8.29 Length: 2402
Score: 54.00 Matches: 10
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Query Match: 100.0% Indels: 0
DB: 17 Gaps: 0

US-09-581-651D-41 (1-10) x US-11-193-789-26 (1-2402)

Qy 1 ValSerIleProProArgAsnLeuGlyTyr 10
|||||
Db 2208 GTGAGTATCCACCCAGAAACCTTGGATAC 2237

RESULT 4
US-11-193-806-26
; Sequence 26, Application US/11193806
; Publication No. US20060024724A1
; GENERAL INFORMATION:
; APPLICANT: Husa, Robert
; APPLICANT: Fisher-Colbrie, Mark
; APPLICANT: LaPointe, Jerome
; APPLICANT: Shorter, Simon
; TITLE OF INVENTION: Oncofetal Fibronectin as a Marker for Health and Disease
; FILE REFERENCE: 17101-028001/829
; CURRENT APPLICATION NUMBER: US/11/193,806
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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(without alignments)
5217.711 Million cell updates/sec

Title: US-09-581-651D-41

Perfect score: 54

Sequence: 1 VSIPPNLGY 10

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	471	7	US-10-242-535A-42467 Sequence 42467, A
2	54	100.0	471	7	US-10-085-783A-42467 Sequence 42467, A
3	54	100.0	600	9	US-10-956-157-9523 Sequence 9523, Ap
4	54	100.0	2127	6	US-10-210-120-49 Sequence 49, Appl
5	54	100.0	2127	9	US-10-956-157-4288 Sequence 4288, Ap
6	54	100.0	2127	9	US-10-909-035-49 Sequence 49, Appl
7	54	100.0	2443	7	US-10-741-601-70 Sequence 70, Appl

8	54	100.0	2443	8	US-10-741-600-238 Sequence 238, App
9	54	100.0	2488	7	US-10-741-601-75 Sequence 75, Appl
10	54	100.0	2488	8	US-10-741-600-244 Sequence 244, App
11	54	100.0	4295	6	US-10-144-194A-51 Sequence 51, Appl
12	54	100.0	4295	8	US-10-491-566-51 Sequence 51, Appl
13	54	100.0	87467	7	US-10-741-601-5634 Sequence 5634, Ap
14	54	100.0	87467	8	US-10-741-601-17624 Sequence 174961, A
c 15	43	79.6	3186778	5	US-10-027-632-174961 Sequence 174961, A
c 16	43	79.6	3186778	6	US-10-027-632-174961 Sequence 174961, A
c 17	42	77.8	25	9	US-10-956-157-202014 Sequence 202014, A
c 18	42	77.8	418	8	US-10-425-115-131037 Sequence 131037, A
c 19	42	77.8	613	4	US-09-925-065A-834813 Sequence 834813, A
c 20	42	77.8	616	4	US-09-925-065A-829110 Sequence 829110, A
c 21	42	77.8	617	4	US-09-925-065A-840083 Sequence 840083, A
c 22	42	77.8	2234	3	US-09-813-153-52 Sequence 52, Appl
c 23	42	77.8	2234	4	US-09-949-925-52 Sequence 52, Appl
c 24	42	77.8	8628	3	US-09-960-706-952 Sequence 952, App
c 25	42	77.8	8628	3	US-09-873-319-622 Sequence 622, App
c 26	42	77.8	8955	10	US-11-097-143-33433 Sequence 33433, A
c 27	41	75.9	399	8	US-10-425-115-36206 Sequence 36206, A
c 28	41	75.9	654	4	US-09-925-065A-835700 Sequence 835700, A
c 29	41	75.9	1110	10	US-11-097-143-15701 Sequence 15701, A
c 30	41	75.9	2285	10	US-11-097-143-28162 Sequence 28162, A
c 31	41	75.9	3330	10	US-11-097-143-15700 Sequence 15700, A
c 32	41	75.9	228139	5	US-10-087-192-232 Sequence 232, App
c 33	40	74.1	492	5	US-10-027-632-281008 Sequence 281008, A
c 34	40	74.1	492	6	US-10-027-632-281008 Sequence 281008, A
c 35	40	74.1	527	4	US-09-925-065A-824091 Sequence 824091, A
c 36	40	74.1	533	4	US-09-925-065A-831462 Sequence 831462, A
c 37	40	74.1	578	4	US-09-925-065A-365691 Sequence 365691, A
c 38	40	74.1	578	7	US-10-424-599-79249 Sequence 79249, A
c 39	40	74.1	662	3	US-09-969-034-815 Sequence 815, App
c 40	40	74.1	677	6	US-10-133-013-21 Sequence 21, Appl
c 41	40	74.1	728	5	US-10-027-632-99730 Sequence 99730, A
c 42	40	74.1	728	6	US-10-027-632-99730 Sequence 99730, A
c 43	40	74.1	941	10	US-11-097-143-11702 Sequence 11702, A
c 44	40	74.1	1480	6	US-10-104-047-128 Sequence 128, App
c 45	40	74.1	1542	9	US-10-997-844-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-10-242-535A-42467
; Sequence 42467, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42467
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-42467

Alignment Scores:
Pred. No.: 1-29 Length: 471
Score: 54.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-581-651D-41 (1-10) x US-10-242-535A-42467 (1-471)

Qy 1 ValSerIleProProArgAsnLeuGlyTyr 10
Db 393 GTGAGTATCCACCCAGAAACCTTGGATAC 422

RESULT 2
US-10-085-783A-42467
; Sequence 42467, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42467
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)-(7)
; OTHER INFORMATION: n is a, c, g, or t

US-10-085-783A-42467

Alignment Scores:
Pred. No.: 1-29 Length: 471
Score: 54.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-581-651D-41 (1-10) x US-10-085-783A-42467 (1-471)

Qy 1 ValSerIleProProArgAsnLeuGlyTyr 10
Db 393 GTGAGTATCCACCCAGAAACCTTGGATAC 422

RESULT 3
US-10-956-157-9523
; Sequence 9523, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9523
; LENGTH: 600

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9523

Alignment Scores:
Pred. No.: 1-65 Length: 600
Score: 54.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
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US-09-581-651D-41 (1-10) x US-10-956-157-9523 (1-600)

Qy 1 ValSerIleProProArgAsnLeuGlyTyr 10
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RESULT 4
US-10-210-120-49
; Sequence 49, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 2127
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-210-120-49

Alignment Scores:
Pred. No.: 5-95 Length: 2127
Score: 54.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-581-651D-41 (1-10) x US-10-210-120-49 (1-2127)

Qy 1 ValSerIleProProArgAsnLeuGlyTyr 10
Db 1953 GTGAGTATCCACCCAGAAACCTTGGATAC 1982

RESULT 5
US-10-956-157-4288
; Sequence 4288, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4288
; LENGTH: 2127
; TYPE: DNA

GenCore version 5.1.8
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Title: US-09-581-651D-41
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Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abs/ABSSWEB spaol/US09581651/runat 10052006 181213 253/app query fasta_1
-DB=Issued Patents NA -OFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-HOST=abs804 -USER=US09581651 @CGN 1 1 237 @runat 10052006 181213 253 -NCPU=6
-ICPU=3 -NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	41	75.9	601	3	US-09-949-016-154321
2	41	75.9	601	3	US-09-949-016-154322
3	41	75.9	601	3	US-09-949-016-154323
4	41	75.9	212139	3	US-09-949-016-16065
C 5	40	74.1	426	3	US-09-621-976-16065
C 6	40	74.1	449	3	US-09-621-976-19043
C 7	40	74.1	1480	3	US-10-104-047-128
C 8	40	74.1	1930	3	US-09-919-172-3
C 9	40	74.1	1930	3	US-09-976-594-957

10	40	74.1	26086	3	US-09-949-016-15355	Sequence 15355, A
11	40	74.1	26238	3	US-09-949-016-12314	Sequence 12314, A
12	39	72.2	601	3	US-09-949-016-105318	Sequence 105318, A
C 13	39	72.2	3003	3	US-08-915-337-1	Sequence 1, Appli
C 14	39	72.2	19818	3	US-09-949-016-12198	Sequence 12198, A
C 15	39	72.2	19819	3	US-09-949-016-16987	Sequence 16987, A
16	39	72.2	41617	3	US-09-949-016-14356	Sequence 14356, A
17	39	72.2	41618	3	US-09-949-016-14356	Sequence 14356, A
18	39	72.2	58108	3	US-09-949-016-13383	Sequence 13383, A
C 19	39	72.2	231129	3	US-09-949-016-16110	Sequence 16110, A
C 20	39	72.2	266293	3	US-09-949-016-11934	Sequence 11934, A
21	38	70.4	502	3	US-09-270-767-6425	Sequence 6425, Ap
22	38	70.4	502	3	US-09-270-767-21707	Sequence 21707, A
23	38	70.4	601	3	US-09-949-016-27189	Sequence 27189, A
C 24	38	70.4	601	3	US-09-949-016-40844	Sequence 40844, A
C 25	38	70.4	601	3	US-09-949-016-40845	Sequence 40845, A
C 26	38	70.4	601	3	US-09-949-016-135102	Sequence 135102, A
C 27	38	70.4	601	3	US-09-949-016-182406	Sequence 182406, A
C 28	38	70.4	601	3	US-09-949-016-200981	Sequence 200981, A
29	38	70.4	607	3	US-09-270-767-10444	Sequence 10444, A
30	38	70.4	780	3	US-09-540-236-1835	Sequence 1835, Ap
31	38	70.4	807	3	US-09-252-991A-11725	Sequence 11725, A
32	38	70.4	918	3	US-10-369-800-1	Sequence 1, Appli
33	38	70.4	1056	3	US-09-252-991A-11806	Sequence 11806, A
34	38	70.4	1503	3	US-10-142-231-48	Sequence 48, Appl
35	38	70.4	1694	6	PCT-US95-04910-9	Sequence 9, Appli
36	38	70.4	3336	2	US-08-368-803-6	Sequence 6, Appli
C 37	38	70.4	3395	9	5223424-11	Patent No. 5223424
38	38	70.4	5153	6	PCT-US95-04910-8	Sequence 8, Appli
39	38	70.4	5426	2	US-08-663-566A-3	Sequence 3, Appli
40	38	70.4	5426	2	US-08-023-610-3	Sequence 3, Appli
41	38	70.4	5426	2	US-08-288-065A-3	Sequence 3, Appli
42	38	70.4	5426	2	US-08-362-240A-3	Sequence 3, Appli
43	38	70.4	5426	3	US-08-804-372A-1	Sequence 1, Appli
44	38	70.4	5426	6	PCT-US95-10245-3	Sequence 3, Appli
45	38	70.4	6220	3	US-09-600-087-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-949-016-154321
; Sequence 154321, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 154321
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-154321

Alignment Scores:
Pred. No.: 91.4
Length: 601
Matches: 7
Score: 41.00
Percent Similarity: 100.0%
Best Local Similarity: 87.5%
Query Match: 75.9%
Indels: 0
Gaps: 0

US-09-581-651D-41 (1-10) x US-09-949-016-154321 (1-601)

QY 2 SerIleProProArgAsnLeuGly 9
Db 117 AGCATACCACCCAGGAATATGGG 140

RESULT 2

US-09-949-016-154322
; Sequence 154322, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 154322
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-154322

Alignment Scores:
Pred. No.: 91.4 Length: 601
Score: 41.00 Matches: 7
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 87.5% Mismatches: 0
Query Match: 75.9% Indels: 0
DB: 3 Gaps: 0

US-09-581-651D-41 (1-10) x US-09-949-016-154322 (1-601)

QY 2 SerIleProProArgAsnLeuGly 9
Db 32 AGCATACCACCCAGGAATATGGG 55

RESULT 3

US-09-949-016-154323
; Sequence 154323, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 154323
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-154323

Alignment Scores:
Pred. No.: 91.4 Length: 601
Score: 41.00 Matches: 7

Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 87.5% Mismatches: 0
Query Match: 75.9% Indels: 0
DB: 3 Gaps: 0

US-09-581-651D-41 (1-10) x US-09-949-016-154323 (1-601)

QY 2 SerIleProProArgAsnLeuGly 9
Db 6 AGCATACCACCCAGGAATATGGG 29

RESULT 4

US-09-949-016-16065
; Sequence 16065, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16065
; LENGTH: 212139
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16065

Alignment Scores:
Pred. No.: 6.69e+04 Length: 212139
Score: 41.00 Matches: 7
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 87.5% Mismatches: 0
Query Match: 75.9% Indels: 0
DB: 3 Gaps: 0

US-09-581-651D-41 (1-10) x US-09-949-016-16065 (1-212139)

QY 2 SerIleProProArgAsnLeuGly 9
Db 150438 AGCATACCACCCAGGAATATGGG 150461

RESULT 5

US-09-621-976-19038/c
; Sequence 19038, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 19038
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-19038

Alignment Scores:
Pred. No.: 95.6 Length: 426
Score: 40.00 Matches: 6

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 12, 2006, 10:25:20 ; Search time 144.264 Seconds
(without alignments)
4864.742 Million cell updates/sec

Title: US-09-581-651D-41

Perfect score: 54

Sequence: 1 VSIPPNLGY 10

Scoring table:

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abs/ABSSWEB.spool/US09581651/runat.10052006.181209.176/app.query.fasta.1
-DB=EST -OPMT=fastap -SUFFIX=p2n.rst -MINMATCH=0 -LOOPEL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs03h
-USER=US09581651 @CGN 1.1.6731 @runat.10052006.181209.176 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
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4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
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6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
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6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	54	100.0	362	1	AI263888
C 2	54	100.0	391	1	AA234360
C 3	54	100.0	440	1	AI754331
C 4	54	100.0	670	5	BU620723
C 5	54	100.0	706	3	BM674187
C 6	54	100.0	747	6	CA423317
C 7	54	100.0	967	5	BX402381

C 8	54	100.0	1044	5	BX398837
C 9	54	100.0	1052	5	BX380582
C 10	46	85.2	238	2	BF757788
C 11	45	83.3	216	8	DR950135
C 12	45	83.3	333	8	DR926919
C 13	45	83.3	455	1	AA797190
C 14	45	83.3	716	8	DR951381
C 15	45	83.3	723	5	BX092161
C 16	45	83.3	778	8	DR923528
C 17	45	83.3	800	8	DR947777
C 18	45	83.3	913	8	DR647139
C 19	44	81.5	890	9	CC480099
C 20	44	81.5	935	10	AG882568
C 21	43	79.6	188	8	DN498580
C 22	43	79.6	237	7	CV191597
C 23	43	79.6	282	1	AV079208
C 24	43	79.6	363	3	BP634715
C 25	43	79.6	442	7	CN963693
C 26	43	79.6	482	9	B46912
C 27	43	79.6	591	9	BZ191710
C 28	43	79.6	653	9	AZ566286
C 29	43	79.6	694	10	AG102718
C 30	43	79.6	756	3	BQ217931
C 31	43	79.6	785	6	CB990018
C 32	43	79.6	811	8	DR838506
C 33	43	79.6	814	8	CX795219
C 34	43	79.6	865	10	AG834589
C 35	43	79.6	866	7	CJ029932
C 36	43	79.6	869	8	CX408686
C 37	43	79.6	873	8	DR451282
C 38	43	79.6	896	10	CL722789
C 39	43	79.6	905	8	DR467514
C 40	43	79.6	909	8	DN026258
C 41	43	79.6	923	7	CF993900
C 42	43	79.6	923	8	DR472075
C 43	43	79.6	945	5	BQ855747
C 44	43	79.6	962	10	CL137507
C 45	43	79.6	1169	8	DR142066

ALIGNMENTS

RESULT 1
AI263888/c
LOCUS
DEFINITION
AI263888 362 bp mRNA linear EST 13-NOV-1998
gi08d11.x1 Soares NHMPu S1 Homo sapiens cDNA clone IMAGE:1855893
3' similar to gb:X02761_cds1 FIBRONECTIN PRECURSOR (HUMAN);, mRNA
sequence.
AI263888.1 GI:3872091
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 362)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. .362
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1855893"
/tissue_type="Pooled human melanocyte, fetal heart, and

pregnant uterus"
/lab_host="DH10B"
/clone_lib="Soares_NhMPu_S1"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NBHPU, and fetal heart NBHH19W) were mixed, and as circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

ORIGIN

Alignment Scores:
Pred. No.: 9.66 Length: 362
Score: 54.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-09-581-651D-41 (1-10) x AI236388 (1-362)

QY 1 ValSerIleProProArgAsnLeuGlyTyr 10
|||||

Db 184 GTGAGTATCCCAACCTTGGATAC 155
|||||

RESULT 2
AA234360/c
LOCUS
DEFINITION
AA234360.1 Soares_NhMPu_S1 Homo sapiens cDNA clone IMAGE:668930 3'
similar to gb:X02761_cds1 FIBRONECTIN PRECURSOR (HUMAN); mRNA
sequence.
ACCESSION
AA234360 GI:1858635
VERSION
AA234360.1
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 391)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 678 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 376.
Location/Qualifiers
1..391
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5562897"
/db_xref="taxon:9606"
/clone="IMAGE:668930"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/clone_lib="Soares_NhMPu_S1"

pregnant uterus"
/lab_host="DH10B"
/clone_lib="Soares_NhMPu_S1"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NBHPU, and fetal heart NBHH19W) were mixed, and as circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

ORIGIN

Alignment Scores:
Pred. No.: 10.5 Length: 391
Score: 54.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-09-581-651D-41 (1-10) x AA234360 (1-391)

QY 1 ValSerIleProProArgAsnLeuGlyTyr 10
|||||

Db 175 GTGAGTATCCCAACCTTGGATAC 146
|||||

RESULT 3
AI754331/c
LOCUS
DEFINITION
AI754331.1 Human bone marrow stromal cells Homo sapiens cDNA clone
HBMSC cr23e08 3', mRNA sequence.
ACCESSION
AI754331 GI:5132595
VERSION
AI754331.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 440)
Jia,L., Young,M.F., Powell,J., Yang,L., Ho,N.C., Hotchkiss,R.,
Robey,P.G. and Francomano,C.A.
Gene expression profile of human bone marrow stromal cells:
high-throughput expressed sequence tag sequencing analysis
Genomics 79 (1), 7-17 (2002)
11827452
Contact: Libin Jia
Medical Genetics Branch
National Human Genome Research Institute
10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
Tel: 301-402-4877
Fax: 301-496-7157
Email: libin@helix.nih.gov
DNA Sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).
Plate: 23 row: e Column: 08
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
1..440
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HBMSC_cr23e08"
/sex="mixed"
/tissue_type="bone marrow stroma"
/dev_stages="mixed"
/lab_host="XLI-Blue MRF"/SOLR"
/clone_lib="Human bone marrow stromal cells"
/note="Vector: pBluescript; Site 1: EcoRI; Site 2: XhoI;
mRNA made from human bone marrow stroma, cDNA made by
oligo-dT priming. Directionally cloned. Size-selected for
average insert size >0.5 kb. Library constructed by Dr.

GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 12, 2006, 09:52:22 ; Search time 16.1963 Seconds
(without alignments)
6172.414 Million cell updates/sec

Title: US-09-581-651d-41
Perfect score: 54
Sequence: 1 VSIPPRNLGY 10

Scoring table:
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/abs/ABSSWEB.spool/US09581651/runat_10052006_181204_141/app.query.fasta.1
-DB=N Geneseq -QFWT=fastcap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bloum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptco -NORW=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs03p
-USER=US09581651 @CGN_1_1_1359 @runat_10052006_181204_141 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 21:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*
- 14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	1929	13	ADSL17488
2	54	100.0	1929	13	ADR97657
3	54	100.0	1929	14	ADW4479
4	54	100.0	1929	14	ADY55703

5	54	100.0	1929	14	ADY32457	Ady32457 Human fib
6	54	100.0	1929	14	AEBS6257	Aeb56257 Event seq
7	54	100.0	1929	14	AEBS78061	Aeb78061 Human DNA
8	54	100.0	2137	10	ADD18477	Add18477 Human pro
9	54	100.0	2147	2	AA81299	Aax81299 Human mig
10	54	100.0	2358	13	ADR67201	Adr67201 Human bla
11	54	100.0	2402	14	AD226738	Adz26738 Human fib
12	54	100.0	2443	13	ADQ38575	Adq38575 Human SNP
13	54	100.0	2488	13	ADQ38581	Adq38581 Human SNP
14	54	100.0	4295	8	ACC72037	Acc72037 BC00770 g
15	54	100.0	11026	4	AAK72958	Aak72958 Human imm
16	54	100.0	31749	4	AAK72959	Aak72959 Human imm
17	54	100.0	78925	3	AAC89888	Aac89888 Human FN
c 18	45	83.3	79084	12	ADQ97563	Adq97563 Human can
c 19	44	81.5	28564	10	ADD47028	Add47028 Human gen
c 20	42	77.8	792	11	ACL32370	ACL32370 Rice abio
c 21	42	77.8	2234	2	AAZ00451	Aaz00451 Human sec
c 22	42	77.8	2234	10	ADA56384	Ada56384 Gene enco
c 23	42	77.8	8628	6	ABK64727	Abk64727 Human ben
c 24	42	77.8	8955	4	ABL24128	AbL24128 Drosophil
c 25	41	75.9	574	13	ADQ56307	Adq56307 Novel can
c 26	41	75.9	1110	4	ABL12307	AbL12307 Drosophil
c 27	41	75.9	2285	4	ABL20614	AbL20614 Drosophil
c 28	41	75.9	3330	4	ABL12306	AbL12306 Drosophil
c 29	41	75.9	228139	11	ACN44002	Acn44002 Human gen
c 30	40	74.1	480	10	ACD98232	AcD98232 Human col
c 31	40	74.1	662	6	ABQ57120	Abq57120 Human col
c 32	40	74.1	677	10	ADI02480	Adi02480 Human CDN
c 33	40	74.1	941	4	ABL09641	AbL09641 Drosophil
c 34	40	74.1	1480	10	ADB61974	AdB61974 Human CDN
c 35	40	74.1	1542	14	AEA18948	Aea18948 Methylo
c 36	40	74.1	1752	13	ADX63544	Adx63544 Plant ful
c 37	40	74.1	1906	8	ABX12015	Abx12015 Prostate
c 38	40	74.1	1930	6	ABS62728	Abs62728 Transact
c 39	40	74.1	1930	12	ADL13228	AdL13228 Human ste
c 40	40	74.1	1930	14	ADV85752	Adv85752 Human DNA
c 41	40	74.1	1964	6	AAS94775	Aas94775 Human DNA
c 42	40	74.1	2288	4	ABL21423	AbL21423 Drosophil
c 43	40	74.1	2417	12	ADM91237	Adm91237 DNA homol
c 44	40	74.1	2417	14	ADW13961	Adw13961 Mouse CDN
c 45	40	74.1	2943	4	ABL18172	AbL18172 Drosophil

ALIGNMENTS

RESULT 1	
ADSL17488	
ID	ADSL17488 standard; DNA; 1929 BP.
XX	
AC	ADSL17488;
XX	
DT	02-DRC-2004 (first entry)
XX	
DE	Nucleotide sequence of human fibronectin 1.
XX	
KW	cell state; time-lapse profile; protein-protein interaction;
KW	drug screening; cancer; infectious disease; allergy; hypertension;
KW	hyperlipaemia; diabetes; cardiac disease; cerebral infarction; dementia;
KW	obesity; arteriosclerosis; infertility; mental disease; nervous disease;
KW	cataract; progeria; hypersensitivity; ultraviolet radiation; human;
KW	fibronectin 1; actin acting substance; transfection array; gene; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..1929
FT	/*tag= a
FT	/product= "fibronectin 1"
XX	
PN	WO2004079007-A2.
XX	
PD	16-SEP-2004.
XX	

PF 03-MAR-2004; 2004WO-JP002694.
XX
XX
XX 04-MAR-2003; 2003JP-00057870.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
XX Miyake M, Yoshikawa T, Uchimura E, Miyake J;
PI WPI; 2004-662438/64.
DR P-PSDB; ADS17489.
XX
XX Presenting a state of a cell, useful for diagnosing and treating a
PT disease, e.g. cancer, infectious disease, allergy, diabetes, dementia,
PT obesity, infertility, or cataract, comprises obtaining a time-lapse
PT profile of the cell.
XX
XX Disclosure; SEQ ID NO 1; 532pp; English.
XX
XX The specification describes a method and system for accurately presenting
CC a state of a cell. The method comprises obtaining a time-lapse profile of
CC the cell by time-lapse monitoring of a gene state associated with at
CC least one gene derived from the cell, and presenting the time-lapse
CC profile. The gene comprises a transcription control sequence, and the
CC gene state includes expression of the gene. The method and system are
CC useful presenting a state of a cell. The method can allow the elucidation
CC of key protein-protein interactions suitable for targeting by drug
CC screening protocols. The method is useful for diagnosing or treating a
CC disease, e.g. cancer, infectious disease due to viruses or bacteria,
CC allergy, hypertension, hyperlipaemia, diabetes, cardiac disease, cerebral
CC infarction, dementia, obesity, arteriosclerosis, infertility, mental and
CC nervous diseases, cataract, progeria, or hypersensitivity to ultraviolet
CC radiation. The present sequence encodes human fibronectin 1. Bovine
CC fibronectin was used as a candidate for an actin acting substance. The
CC actin acting substance was used with transfection reagents and amplified
CC plasmid DNA in assays using transfection arrays, in the course of the
CC invention.
XX
XX SQ Sequence 1929 BP; 507 A; 462 C; 544 G; 416 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.69 Length: 1929
Score: 54.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0

US-09-581-651D-41 (1-10) x ADS17488 (1-1929)
QY 1 ValSerIleProProArgAsnLeuGlyTyr 10
Db 1897 GTGAGTATCCCAACCCAGAAACCTTGGATAC 1926

RESULT 2
ADR97657
ID ADR97657 standard; DNA; 1929 BP.
XX ADR97657;
XX
XX 02-DEC-2004 (first entry)
DT Human fibronectin 1 DNA, an actin acting substance SeqID 1.
DE human; gene; ds; transfection efficiency; actin acting substance;
XX extracellular matrix; fibronectin 1; gene introduction reagent.
KW
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 1..1929
FT /*tag= a
FT /product= "Fibronectin protein"
XX

PN WO2004079332-A2.
XX
XX 16-SEP-2004.
PD
XX 03-MAR-2004; 2004WO-JP002696.
XX
XX 04-MAR-2003; 2003JP-00057869.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA
XX Miyake M, Yoshikawa T, Uchimura E, Miyake J;
PI WPI; 2004-677173/66.
DR P-PSDB; ADR97658.
XX
XX Composition comprising an actin acting substance or an actin acting
PT substance and a target substance, useful for increasing the efficiency of
PT introducing a target substance into a cell and in cell biology or genetic
PT engineering.
XX
XX Claim 4; SEQ ID NO 1; 347pp; English.
XX
XX This invention relates to a novel composition and method for increasing
CC the efficiency of introducing a target substance into a cell.
CC Specifically, it refers to the introduction of DNA (e.g. the gene of
CC interest to be transfected), polypeptides, sugars or complexes thereof
CC into a cell, and comprises an actin acting substance. The present
CC invention describes the actin acting substance as an extracellular matrix
CC protein, a variant or fragment thereof selected from fibronectin, laminin
CC or vitronectin. The composition further comprises a gene introduction
CC reagent selected from cationic polymers, cationic lipids, and calcium
CC phosphate, as well as a gold colloid particle that is contacted with the
CC cell. As such, the composition, kit, device or method is useful for
CC increasing the efficiency of introducing a target substance into a cell
CC and thus is useful in the fields of cell biology, genetic engineering and
CC molecular biology. This polynucleotide sequence is the human fibronectin
CC DNA sequence of the invention.
XX
XX SQ Sequence 1929 BP; 507 A; 462 C; 544 G; 416 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.69 Length: 1929
Score: 54.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0

US-09-581-651D-41 (1-10) x ADR97657 (1-1929)
QY 1 ValSerIleProProArgAsnLeuGlyTyr 10
Db 1897 GTGAGTATCCCAACCCAGAAACCTTGGATAC 1926

RESULT 3
ADM44479
ID ADM44479 standard; DNA; 1929 BP.
XX ADM44479;
XX
XX 24-MAR-2005 (first entry)
DT Human fibronectin 1 DNA.
DE cell transduction; nerves; cell adhesion; fibronectin 1; ds; gene.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 1..1929
FT /*tag= a
FT /product= "fibronectin 1"
XX

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 12, 2006, 10:13:41 ; Search time 184.709 Seconds
(without alignments)
4616.200 Million cell updates/sec

Title: US-09-581-651D-41
Perfect score: 54
Sequence: 1 VSIPRNLGY 10

Scoring table:
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 117666282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abs/ABSSWEB pool/US09581651/runat_10052006_181206_153/app_query.fasta.1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs04
-USER=US09581651 @CGN 1.1 5142 @runat_10052006_181206_153 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	471	6	CQ697541 Sequence
2	54	100.0	1929	6	CQ871810 Sequence
3	54	100.0	1929	6	CQ871828 Sequence

4	54	100.0	2147	6	BD137021	BD137021 Polypepti
5	54	100.0	2147	6	AX003229	AX003229 Sequence
6	54	100.0	2147	8	HS276395	HS276395 Homo sapi
7	54	100.0	2192	8	HS253086	HS253086 Homo sapi
8	54	100.0	2358	6	CQ875358	CQ875358 Sequence
9	54	100.0	4321	8	HS2806214	HS2806214 Homo sapi
10	54	100.0	5984	8	AJ849445	AJ849445 Homo sapi
c 11	54	100.0	143947	8	AC012462	AC012462 Homo sapi
c 12	49	90.7	110000	14	AC106675	AC106675 Rattus no
c 13	47	87.0	24068	14	AC131345	AC131345 Rattus no
c 14	47	87.0	247046	14	AC119441	AC119441 Rattus no
c 15	46	85.2	178271	9	AC091785	AC091785 Genomic s
c 16	45	83.3	6001	5	SQUCARPSYN	L31362 Squallus aca
c 17	45	83.3	9017	8	AL137121	AL137121 Human DNA
c 18	45	83.3	95771	8	AC093891	AC093891 Homo sapi
c 19	45	83.3	139452	9	AL954675	AL954675 Mouse DNA
c 20	45	83.3	150488	8	AL359392	AL359392 Human DNA
c 21	45	83.3	176204	14	AC140804	AC140804 Homo sapi
c 22	45	83.3	181755	14	AC015758	AC015758 Homo sapi
c 23	45	83.3	194093	9	AC139037	AC139037 Mus muscu
c 24	45	83.3	220102	9	AC158152	AC158152 Mus muscu
c 25	45	83.3	236521	14	AC129274	AC129274 Rattus no
c 26	44	81.5	105011	14	AC096724	AC096724 Homo sapi
c 27	44	81.5	110000	1	EX936398	Continuation (38 o
c 28	44	81.5	156278	14	AC015607	AC015607 Homo sapi
c 29	44	81.5	163339	14	AC149785	AC149785 Otolenur
c 30	44	81.5	169649	8	AL133328	AL133328 Human DNA
c 31	44	81.5	171940	14	AC148514	AC148514 Papio anu
c 32	44	81.5	173146	8	AC082649	AC082649 Homo sapi
c 33	44	81.5	180594	9	AC112270	AC112270 Mus muscu
c 34	44	81.5	207362	14	AC156716	AC156716 Bos tauru
c 35	44	81.5	213625	14	AC120950	AC120950 Rattus no
c 36	44	81.5	216381	9	AC120138	AC120138 Mus muscu
c 37	44	81.5	218524	9	AC151721	AC151721 Mus muscu
c 38	44	81.5	224009	14	AC164301	AC164301 Mus muscu
c 39	44	81.5	228405	14	AC123473	AC123473 Rattus no
c 40	44	81.5	241510	14	AC094856	AC094856 Rattus no
c 41	44	81.5	246248	14	AC130847	AC130847 Rattus no
c 42	44	81.5	267540	14	AC107153	AC107153 Rattus no
c 43	43	79.6	1100	13	HIM287013	AC107153 Human imm
c 44	43	79.6	101299	1	AC022423	AC287013 Homo sapi
c 45	43	79.6	110000	1	CP000082	AC022423 Homo sapi

ALIGNMENTS

RESULT 1
CQ697541
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

CQ697541
Sequence
CQ697541
CQ697541.1
GI:42248968
Sequence 42467 from Patent WO02070737.
471 bp
DNA
linear
PAT 03-FEB-2004

Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1
Liew,C.C., Marshall,W.E. and Zhang,H.
Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 42467 12-SEP-2002;
Chondrogene Inc. (CA)

Location/Qualifiers

1..471
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.:

Score:

0.523

Length:

Matches:

54.00

471

10

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Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 6

US-09-581-651D-41 (1-10) x CQ697541 (1-471)

QY 1 ValSerIleProProArgAsnLeuGlyTyr 10
Db 393 GTGAGTATCCACCCAGAAACCTTGGATAC 422

RESULT 2
CQ871810 1929 bp DNA linear PAT 27-SEP-2004
LOCUS Sequence 1 from Patent WO2004079332.
DEFINITION CQ871810
ACCESSION CQ871810
VERSION CQ871810.1 GI:52745842
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Miyake,M.A., Yoshikawa,T.A., Uchimura,E.A. and Miyake,J.A.
TITLE Composition and method for increasing efficiency of introduction of
JOURNAL target substance into cell
Patent: WO 2004079332-A 1 16-SEP-2004;
National Institute of Advanced Industrial Science and Tec hnology
(JP)
FEATURES
source Location/Qualifiers
1..1929
/db_xref="taxon:9606"
CDS
1..1929
/notes="unnamed protein product; fibronectin 1"
/codon_start=1
/protein_id="CAH56867.1"
/db_xref="GI:52745843"
/translation="MLRGPGLLLAVQLGTVAVPSTGASKSKRQAQOMVQPSFVA
VSQKPGCYDNGKHQIINQWERTYLGVALVCTCYGSGRGFNCESKPEAEETCFDKYT
GNTYRGDTERPDKSMIDWCTICAGRGISCTIANRCHGGQSKIGDTRRRPHET
GGVLEPCVLGNGKGEWTKPIAEKCFDHAAGTSYVVGTEWKPQGMWVDTCLGE
SGRITCTSRNCNDQRTSYRIGDTNSKDNRLQICITGNGRGWKCERTHSV
QTSSGSGFTDRAAVYQPPHPQPPYGHCVTDSGVVSYGMQLTKYQGNKQMLCT
CLNGVSCQETAVTQYGGNSGEPCLPFTYNGRTDSTTSNYEQDQKYSFCTDHTVL
VOTRGNSGALCHFPFLYNNHNTDCTSEGRDNMKWCTGTTQNTYDADQKFGFCPMAA
HEEICTTNEGVMYRIGDQKHDMGHMRCCTCVNGRGWETCIAYSQLRDCIYDDI
TYNVNDTFHKEEGHMLNCTCFGQGRGKCDPVDQCDSTGTGYQIGDSWEKVVH
GVRXCYCYGRGIGWHCQPLQTYPSSSGPVEVFTITPSPQNSHPIQWNAPOPSHIS
KYLWRPVSIPRNLGY"
ORIGIN
Alignment Scores:
Pred. No.: 2.15 Length: 1929
Score: 54.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0
US-09-581-651D-41 (1-10) x CQ871828 (1-1929)
QY 1 ValSerIleProProArgAsnLeuGlyTyr 10
Db 1897 GTGAGTATCCACCCAGAAACCTTGGATAC 1926

RESULT 4
CQ871828 2147 bp DNA linear PAT 18-SEP-2002
LOCUS BDI37021
DEFINITION Polypeptides, polynucleotides and uses thereof.
ACCESSION BDI37021
VERSION BDI37021.1 GI:323231966
KEYWORDS JP 2002508179-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 2147)
AUTHORS Schor,S.L. and Schor,A.M.
TITLE Polypeptides, polynucleotides and uses thereof
JOURNAL Patent: JP 2002508179-A 1 19-MAR-2002;
UNIVERSITY OF DUNDEE
COMMENT OS Homo sapiens (human)
PN JP 2002508179-A/1
PD 19-MAR-2002
PF 15-DEC-1998 JP 2000539133
PR 16-DEC-1997 GB 9726539.1
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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 10, 2006, 19:42:45 ; Search time 0.598159 Seconds
(without alignments)
784.888 Million cell updates/sec

Title: US-09-581-651D-41

Perfect score: 54

Sequence: 1 VSIPPRNLGY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB.pep.1*
- 2: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep.1*
- 3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pep.1*
- 4: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB.pep.1*
- 5: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB.pep.1*
- 6: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep.1*
- 7: /SIDSS/ptodata/2/pubpaa/US03_NEW_PUB.pep.1*
- 8: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep.1*
- 9: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep.1*
- 10: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep.1*
- 11: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep.1*
- 12: /SIDSS/ptodata/2/pubpaa/US60_NEW_PUB.pep.1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	642	9	US-10-995-561-631
2	54	100.0	657	9	US-10-995-561-622
3	54	100.0	657	11	US-11-193-561-27
4	54	100.0	657	11	US-11-193-771-27
5	54	100.0	657	11	US-11-193-806-27
6	54	100.0	657	11	US-11-193-806-27
7	54	100.0	657	11	US-11-193-857-27
8	39	72.2	454	11	US-11-188-298-2724
9	37	68.5	3482	11	US-11-087-099-2068
10	37	68.5	3488	11	US-11-087-099-9005
11	36	66.7	315	11	US-11-188-298-11717
12	36	66.7	3487	11	US-11-087-099-9068
13	36	66.7	3487	11	US-11-087-099-10423
14	35	64.8	132	11	US-11-188-298-18528
15	35	64.8	327	11	US-11-096-568A-11342
16	35	64.8	342	11	US-11-188-298-14861
17	35	64.8	374	11	US-11-096-568A-11341
18	35	64.8	400	11	US-11-096-568A-11340
19	35	64.8	436	11	US-11-188-298-3852
20	35	64.8	438	11	US-11-188-298-4885
21	35	64.8	432	11	US-11-188-298-5798

ALIGNMENTS

RESULT 1

US-10-995-561-631
; Sequence 631, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 631
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-631

Query Match 100.0%; Score 54; DB 9; Length 642;

Best Local Similarity 100.0%; Pred. No. 0.043;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSIPPRNLGY 10
Db 633 VSIPPRNLGY 642

RESULT 2

US-10-995-561-622
; Sequence 622, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 622

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; LENGTH: 657
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-622

Query Match      100.0%; Score 54; DB 9; Length 657;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VSIPPRNLGY 10
Db      648 VSIPPRNLGY 657

RESULT 3
US-11-193-561-27
; Sequence 27, Application US/11193561
; Publication No. US20060024757A1
; GENERAL INFORMATION:
; APPLICANT: Hussa, Robert
; APPLICANT: Shorter, Simon
; TITLE OF INVENTION: Detection of Oncofetal Fibronectin for Selection of Concepti
; FILE REFERENCE: 17101-080001/831
; CURRENT APPLICATION NUMBER: US/11/193,561
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank NM 054034
; DATABASE ENTRY DATE: 2005-06-10
US-11-193-561-27

Query Match      100.0%; Score 54; DB 11; Length 657;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VSIPPRNLGY 10
Db      648 VSIPPRNLGY 657

RESULT 4
US-11-193-771-27
; Sequence 27, Application US/11193771
; Publication No. US20060024722A1
; GENERAL INFORMATION:
; APPLICANT: Fisher-Colbrie, Mark
; APPLICANT: Hickok, Durlin
; APPLICANT: LaPointe, Jerome P.
; TITLE OF INVENTION: Samples for Detection of Oncofetal Fibronectin and uses thereof
; FILE REFERENCE: 17101-027001/828
; CURRENT APPLICATION NUMBER: US/11/193,771
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30

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; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank NM 054034
; DATABASE ENTRY DATE: 2005-06-10
US-11-193-771-27

Query Match      100.0%; Score 54; DB 11; Length 657;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VSIPPRNLGY 10
Db      648 VSIPPRNLGY 657

RESULT 5
US-11-193-789-27
; Sequence 27, Application US/11193789
; Publication No. US20060024723A1
; GENERAL INFORMATION:
; APPLICANT: Hussa, Robert
; APPLICANT: Fisher-Colbrie, Mark
; APPLICANT: LaPointe, Jerome
; APPLICANT: Senyvel, Andrew
; APPLICANT: Shorter, Simon
; TITLE OF INVENTION: Methods for detecting Oncofetal Fibronectin
; FILE REFERENCE: 17101-029001/830
; CURRENT APPLICATION NUMBER: US/11/193,789
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank NM 054034
; DATABASE ENTRY DATE: 2005-06-10
US-11-193-789-27

Query Match      100.0%; Score 54; DB 11; Length 657;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VSIPPRNLGY 10
Db      648 VSIPPRNLGY 657

RESULT 6
US-11-193-806-27
; Sequence 27, Application US/11193806
; Publication No. US20060024724A1
; GENERAL INFORMATION:

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2006, 19:41:10 ; Search time 3.78834 Seconds
(without alignments)
1102.934 Million cell updates/sec

Title: US-09-581-651D-41

Perfect score: 54

Sequence: 1 VSIPPRNLGY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	642	4	US-10-741-601-354
2	54	100.0	642	5	US-10-741-600-1066
3	54	100.0	657	4	US-10-741-601-359
4	54	100.0	657	5	US-10-741-600-1072
5	38	70.4	70	4	US-10-425-115-215232
6	38	70.4	71	4	US-10-424-599-186842
7	38	70.4	89	4	US-10-437-963-179849
8	38	70.4	98	4	US-10-425-115-316330
9	38	70.4	118	4	US-10-425-115-313669
10	38	70.4	145	6	US-11-097-143-40935
11	38	70.4	279	4	US-10-369-800-2
12	38	70.4	291	4	US-10-250-727-4
13	38	70.4	291	4	US-10-250-824-4
14	38	70.4	500	4	US-10-142-231-61
15	38	70.4	500	4	US-10-356-153-61
16	38	70.4	500	5	US-10-884-115-61
17	37	68.5	40	3	US-09-973-278-198
18	37	68.5	41	3	US-09-983-802-211
19	37	68.5	41	3	US-09-984-490-211
20	37	68.5	145	4	US-10-437-963-193731
21	37	68.5	152	4	US-10-425-115-301041
22	37	68.5	485	4	US-10-142-231-88
23	37	68.5	485	4	US-10-356-153-88
24	37	68.5	485	5	US-10-884-115-88
25	37	68.5	485	5	US-10-732-923-1081
26	36	66.7	45	4	US-10-424-599-167062
27	36	66.7	150	5	US-10-450-763-36134

28 36 66.7 154 3 US-09-925-297-783 Sequence 783, Appl
29 36 66.7 216 5 US-10-965-898-1 Sequence 1, Appl
30 36 66.7 512 4 US-10-142-231-87 Sequence 87, Appl
31 36 66.7 512 4 US-10-356-153-87 Sequence 87, Appl
32 36 66.7 512 5 US-10-884-115-87 Sequence 87, Appl
33 36 66.7 578 5 US-10-450-763-32551 Sequence 32551, A
34 36 66.7 738 5 US-10-450-763-38284 Sequence 189959, A
35 36 66.7 771 4 US-10-437-963-189959 Sequence 38284, A
36 36 66.7 822 4 US-10-437-963-104983 Sequence 104983, A
37 36 66.7 1572 6 US-11-097-143-15396 Sequence 15396, A
38 35 64.8 74 4 US-10-425-115-353331 Sequence 353331, A
39 35 64.8 107 4 US-10-425-115-283878 Sequence 283878, A
40 35 64.8 110 4 US-10-437-963-118856 Sequence 118856, A
41 35 64.8 123 4 US-10-425-115-329379 Sequence 329379, A
42 35 64.8 137 4 US-10-437-963-143622 Sequence 143622, A
43 35 64.8 139 4 US-10-437-963-186450 Sequence 186450, A
44 35 64.8 147 4 US-10-437-963-143028 Sequence 143028, A
45 35 64.8 147 5 US-10-450-763-34424 Sequence 34424, A

ALIGNMENTS

RESULT 1

US-10-741-601-354

; Sequence 354, Application US/10741601

; Publication No. US20040166519A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: CLO01500

; CURRENT APPLICATION NUMBER: US/10/741.601

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 26415

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 354

; LENGTH: 642

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-741-601-354

Query Match

Best Local Similarity 100.0%; Score 54; DB 4; Length 642;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSIPPRNLGY 10

Db 633 VSIPPRNLGY 642

RESULT 2

US-10-741-600-1066

; Sequence 1066, Application US/10741600

; Publication No. US20050026169A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: CLO01499

; CURRENT APPLICATION NUMBER: US/10/741.600

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1066

; LENGTH: 642

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-741-600-1066

Query Match

Best Local Similarity 100.0%; Score 54; DB 5; Length 642;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 VSIPPRNLGY 10
      |||||
Db      633 VSIPPRNLGY 642

RESULT 3
US-10-741-601-359
; Sequence 359, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 359
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-359

Query Match      100.0%; Score 54; DB 4; Length 657;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VSIPPRNLGY 10
      |||||
Db      648 VSIPPRNLGY 657

RESULT 4
US-10-741-600-1072
; Sequence 1072, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1072
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1072

Query Match      100.0%; Score 54; DB 5; Length 657;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VSIPPRNLGY 10
      |||||
Db      648 VSIPPRNLGY 657

RESULT 5
US-10-425-115-215232
; Sequence 215232, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; SEQ ID NO 179849

; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 215232
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_127889C.1.pep
US-10-425-115-215232

Query Match      70.4%; Score 38; DB 4; Length 70;
Best Local Similarity 77.8%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 VSIPPRNLG 9
      |
Db      56 VKYPPRNLG 64

RESULT 6
US-10-424-599-186842
; Sequence 186842, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 186842
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_139730C.1.pep
US-10-424-599-186842

Query Match      70.4%; Score 38; DB 4; Length 71;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 PPRNLGY 10
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Db      12 PPRNFGY 18

RESULT 7
US-10-437-963-179849
; Sequence 179849, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 179849
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2006, 19:25:45 ; Search time 1.02761 Seconds
(without alignments)
804.545 Million cell updates/sec

Title: US-09-581-651D-41

Perfect score: 54

Sequence: 1 VSIPPRNLGY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	70.4	148	2	US-09-270-767-42039
2	38	70.4	279	2	US-10-369-800-2
3	38	70.4	351	2	US-09-252-991A-28377
4	38	70.4	500	2	US-10-142-231-61
5	37	68.5	40	2	US-09-973-278-198
6	37	68.5	41	2	US-09-227-357-211
7	37	68.5	485	2	US-10-142-231-88
8	36	66.7	269	2	US-09-949-016-6927
9	36	66.7	497	2	US-09-270-767-62287
10	36	66.7	512	2	US-10-142-231-87
11	36	66.7	729	2	US-09-949-016-11190
12	36	66.7	782	2	US-09-270-767-46675
13	35	64.8	16	2	US-09-809-464-5
14	35	64.8	28	1	US-08-479-275D-17
15	35	64.8	28	1	US-08-479-275D-25
16	35	64.8	28	1	US-08-488-271B-17
17	35	64.8	28	1	US-08-488-271B-25
18	35	64.8	274	2	US-09-252-991A-32312
19	35	64.8	290	2	US-09-107-433-4222
20	35	64.8	315	2	US-09-583-110-4592
21	35	64.8	424	2	US-09-270-767-37179
22	35	64.8	424	2	US-09-270-767-37179
23	35	64.8	492	2	US-10-142-231-60
24	35	64.8	509	2	US-10-142-231-67
25	35	64.8	543	2	US-09-351-150A-15
26	35	64.8	834	2	US-09-198-452A-287
27	35	64.8	839	2	US-09-438-185A-276

28	35	64.8	841	2	US-09-546-990-2	Sequence 2, Appli
29	35	64.8	886	2	US-09-543-681A-4302	Sequence 4302, Ap
30	35	64.8	953	2	US-09-252-991A-21559	Sequence 21559, A
31	34	63.0	72	2	US-09-543-681A-7461	Sequence 7461, Ap
32	34	63.0	77	2	US-09-513-999C-5060	Sequence 5060, Ap
33	34	63.0	109	2	US-09-205-258-694	Sequence 694, App
34	34	63.0	109	2	US-10-004-860-694	Sequence 694, App
35	34	63.0	113	2	US-09-621-976-4206	Sequence 4206, Ap
36	34	63.0	124	2	US-09-513-999C-7059	Sequence 7059, Ap
37	34	63.0	130	2	US-09-434-840-32	Sequence 32, Appl
38	34	63.0	157	2	US-09-364-230-26	Sequence 26, Appl
39	34	63.0	164	2	US-09-270-767-41196	Sequence 41196, A
40	34	63.0	164	2	US-09-270-767-56412	Sequence 56412, A
41	34	63.0	205	2	US-09-252-991A-20776	Sequence 20776, A
42	34	63.0	208	2	US-10-104-047-2284	Sequence 2284, Ap
43	34	63.0	227	2	US-09-270-767-42649	Sequence 42649, A
44	34	63.0	269	2	US-09-630-250B-19	Sequence 19, Appl
45	34	63.0	269	2	US-09-937-919-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-270-767-42039
; Sequence 42039, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 42039
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-42039

Query Match 70.4%; Score 38; DB 2; Length 148;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VSIPPRNLG 9

Db 84 VSIPPPNMG 92

RESULT 2

US-10-369-800-2
; Sequence 2, Application US/10369800
; Patent No. 6897033
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Dawson, Thomas
; APPLICANT: Deangelis, Yvonne
; APPLICANT: Johnstone, Kevin
; APPLICANT: Kaczvinsky, Joseph
; APPLICANT: Saunders, Charles
; APPLICANT: Walter, Richard
; TITLE OF INVENTION: No. 6897033el Fungal Lipase
; FILE REFERENCE: No. 6897033el Fungal Lipase
; CURRENT APPLICATION NUMBER: US/10/369,800
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 279
; TYPE: PRT
; ORGANISM: malassezia globosa
US-10-369-800-2

Query Match 70.4%; Score 38; DB 2; Length 279;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SIPPRNLGY 10
: : : : :
Db 207 TVPPRALGY 215

RESULT 3
US-09-252-991A-28377
; Sequence 28377, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28377
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28377

Query Match 70.4%; Score 38; DB 2; Length 351;
Best Local Similarity 60.0%; Pred. No. 56;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VSIPPRNLGY 10
: : : : :
Db 341 LSLPPAHLGY 350

RESULT 4
US-10-142-231-61
; Sequence 61, Application US/10142231
; Patent No. 6787343
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES AND THEIR USES
; FILE REFERENCE: 62773
; CURRENT APPLICATION NUMBER: US/10/142,231
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: 60/165,250
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Taxus cuspidata
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(500)
; OTHER INFORMATION: "Xaa" equals any peptide
US-10-142-231-61

Query Match 70.4%; Score 38; DB 2; Length 500;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VSIPPRNLGY 10
: : : : :
Db 52 VTLPFGNLGF 61

RESULT 5
US-09-973-278-198
; Sequence 198, Application US/09973278
; Patent No. 6924354
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P2
; CURRENT APPLICATION NUMBER: US/09/973,278
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/239,899
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/227,357
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/13684
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/051,926
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,793
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,925
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,929
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,803
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,732
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,931
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,932
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,916
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,930
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,918
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,920
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,733
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,795
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,919
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,928
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/055,722
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,723
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,948
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,949
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,953
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,950
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,947
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,964
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056,360
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,684
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,984
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: 1997-08-18

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 10, 2006, 19:13:45 ; Search time 4.72393 Seconds
(without alignments)
1493.521 Million cell updates/sec

Title: US-09-581-651D-41
Perfect score: 54
Sequence: 1 VSIPPRNLGY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05_80.*

1: uniprot_sprot.*

2: uniprot_crembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	657	2	Q564H7 HUMAN
2	54	100.0	749	2	Q72391 HOMO SAPIEN
3	42	77.8	775	2	Q4HYV4 GIBBERELLA
4	41	75.9	181	2	Q56F00 CAUD
5	41	75.9	2515	2	Q77365 PLASMIDIUM
6	40	74.1	267	2	Q7R2C3 GIARDIA LAM
7	40	74.1	887	1	SRS2_SCHPO
8	40	74.1	3689	2	Q7PFP9 ANOXA
9	39	72.2	236	2	Q650B9 BACIFR
10	39	72.2	331	2	Q65TX9 MANSIM
11	39	72.2	342	2	Q7SF17 NEUCR
12	39	72.2	411	2	Q4NJ95 ARTHROBACTE
13	39	72.2	454	2	Q4R8B8 BRHOO
14	39	72.2	644	2	Q4S6N4 TETNG
15	39	72.2	1708	2	Q7PVR6 ANOXA
16	38	70.4	145	2	Q9VE17 DROME
17	38	70.4	189	2	Q8BBK5 SHEPC
18	38	70.4	283	2	Q8YBB3 BRUME
19	38	70.4	303	2	Q869A2 ACHTE
20	38	70.4	306	2	Q576Y0 BRUAB
21	38	70.4	306	2	Q8FX28 BRUSU
22	38	70.4	315	2	Q8U7R8 AGRT5
23	38	70.4	337	1	TRUD MANSIM
24	38	70.4	364	2	Q5E0T4 VIBF1
25	38	70.4	824	2	Q7UA91 SYNEX
26	38	70.4	829	2	Q7V9E4 PROMM
27	38	70.4	849	2	Q4FLZ5 GRICK
28	38	70.4	877	2	Q98RX7 GUITH
29	38	70.4	920	1	PARC SYN3
30	38	70.4	1127	1	NUL133 CAEEL
31	37	68.5	186	2	Q84RE9 ARABIDOPSIS

32	37	68.5	243	2	Q6MKQ8 BDEBA	Q6mkq8 bdellovibri
33	37	68.5	297	2	Q9ZV59 ARATH	Q9zv59 arabidopsis
34	37	68.5	321	2	Q7FLJ2 ORYSA	Q7flj2 oryza sativ
35	37	68.5	324	2	Q84RF0 ARATH	Q84rf0 arabidopsis
36	37	68.5	325	2	Q84RF1 ARATH	Q84rf1 arabidopsis
37	37	68.5	372	2	Q9HGV6 ASCO	Q9hgv6 saitoella c
38	37	68.5	391	2	Q6G034 BARQU	Q6g034 bartonella
39	37	68.5	485	1	T13H TAXCU	Q8w4t9 taxus cuspi
40	37	68.5	485	2	Q6G2I3 TAXCU	Q6gz13 taxus cuspi
41	37	68.5	485	2	Q5BU48 CONI	Q5bu48 taxus x med
42	37	68.5	485	2	Q56GD5 TAXCH	Q56gd5 taxus chine
43	37	68.5	515	2	Q5JDQ0 PYRKO	Q5jdq0 pyrococcus
44	37	68.5	624	2	Q4SMS4 TETNG	Q4sms4 tetraodon n
45	37	68.5	792	2	Q6EPG4 ORYSA	Q6epg4 oryza sativ

ALIGNMENTS

RESULT 1
Q564H7 HUMAN PRELIMINARY; PRT; 657 AA.
AC Q564H7;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Migration stimulating factor.
GN Name=FN1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
RX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE
RA Kay R.A., Ellis I.R., Jones S.J., Perrier S., Florence M.M.,
RA Schor A.W., Schor S.L.;
RT "mRNA 3'-UTR truncation: a novel mechanism regulating gene
expression.";
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR SMR; Q564H7; 48-140, 183-275, 305-464.
DR Ensembl; ENSG00000115414; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000083; Fibrinctn1.
DR InterPro; IPR000562; FN_type2_col_bd.
DR InterPro; IPR001724; Glyco_hydro_58.
DR Pfam; PF00039; fn1; 9.
DR Pfam; PF00040; fn2; 2.
DR PRINTS; PR00012; FNTYPEI.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00049; GLHYDLASE58.
DR SMART; SM00058; FN1; 9.
DR SMART; SM00059; FN2; 2.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01253; FN1_1; 9.
DR PROSITE; PS1091; FN1_2; 9.
DR PROSITE; PS00023; FN2_1; 2.
DR PROSITE; PS1092; FN2_2; 2.
KW Repeat.

SQ SEQUENCE 657 AA; 73752 MW; 8CA04E64486ABCD0 CRC64;
Query Match 100.0%; Score 54; DB 2; Length 657;
Best Local Similarity 100.0%; Pred. No. 0.23; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy 1 VSIPPRNLGY 10
|||||
Db 648 VSIPPRNLGY 657

RESULT 2

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Q72391_HUMAN
ID Q72391 HUMAN PRELIMINARY; PRT; 749 AA.
AC Q72391.
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686B18150.
GN Name=DKFZp686B18150;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human colon endothel primary cell culture;
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538045; CAD97984.1; -; mRNA.
DR HSSP; Q96KP7; 1PBR.
DR SMR; Q72391; 140-232, 275-367, 397-556.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008243; F:plasminogen activator activity; IEA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR000083; Fibrinctn1.
DR InterPro; IPR000562; FN Type II.
DR InterPro; IPR001724; Glyco_hydro_58.
DR Pfam; PF00039; fn1; 9.
DR Pfam; PF00040; fn2; 2.
DR PRINTS; PR00012; FNTYPEI.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00849; GLHYDRLASE58.
DR ProDom; PD000995; FN_Type_II_2.
DR SMART; SM00058; FN1; 9.
DR SMART; SM00059; FN2; 2.
DR PROSITE; PS00022; EGF_1; UNKNOWN 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 9.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
KW Hypothetical protein
SQ SEQUENCE 749 AA; 83524 MW; C8DDF97F3ED2F0DE CRC64;

Query Match 100.0%; Score 54; DB 2; Length 749;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSIPPRNLGY 10
Db 740 VSIPPRNLGY 749

RESULT 3
Q4HYV4_GIBZE
ID Q4HYV4_GIBZE PRELIMINARY; PRT; 775 AA.
AC Q4HYV4.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG09854.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgaltier B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,

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RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kanal M., Kanat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramaamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACM01000407; EAA76021.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 775 AA; 85797 MW; 02EFC46C826B4002 CRC64;

Query Match 77.8%; Score 42; DB 2; Length 775;
Best Local Similarity 77.8%; Pred. No. 54;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SIPPRNLGY 10
Db 397 SYPPKNLGY 405

RESULT 4
Q56F00_9CAUD
ID Q56F00_9CAUD PRELIMINARY; PRT; 181 AA.
AC Q56F00.
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein PHG31ORF011c.
GN Name=PHG31ORF011c; ORFNames=PHG31p11;
OS Aeromonas phage 31.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=321023;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nolan J.M., Petrov V., Bertrand C., Krusch H.M., Karam J.D.;
RT "Comparative analysis of the Aeromonas bacteriophage 31 genome.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY962392; AAX63500.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 181 AA; 20612 MW; 21783CD9C2F8C497 CRC64;

Query Match 75.9%; Score 41; DB 2; Length 181;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VSIPPRNLGY 10
Db 89 VVVPFRNWGF 98

RESULT 5
Q77365_PLAF7
ID Q77365_PLAF7 PRELIMINARY; PRT; 2515 AA.
AC Q77365.
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein MAL3P4.16.
GN Name=MAL3P4.16; Synonyms=PRC0485w;

```

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 10, 2006, 19:20:36 ; Search time 0.766871 Seconds
(without alignments)
1254.667 Million cell updates/sec

Title: US-09-581-651D-41
Perfect score: 54
Sequence: 1 VSIPPRNLGY 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	75.9	2523	2 T18477	hypothetical prote
2	40	74.1	887	2 T38885	probable ATP-depen
3	38	70.4	283	2 AB3633	nirv precursor (im
4	38	70.4	315	2 A99192	nirv precursor (AF
5	38	70.4	315	2 A13094	nitrite reductase,
6	38	70.4	877	2 D90086	DNA gyrase A-subun
7	38	70.4	944	2 S75188	DNA topoisomerase
8	38	70.4	1102	2 S44772	C29E4.4 protein -
9	37	68.5	297	2 E84731	hypothetical prote
10	37	68.5	1345	2 S55669	tegument protein 7
11	36	66.7	312	2 T23492	hypothetical prote
12	36	66.7	340	2 T23492	hypothetical prote
13	36	66.7	494	2 T32654	hypothetical prote
14	36	66.7	746	2 AG2039	serine/threonine k
15	36	66.7	1136	2 T30878	dynein heavy chain
16	35.5	65.7	484	2 G86475	unknown protein, 1
17	35	64.8	163	2 H72759	probable dCTP deam
18	35	64.8	238	2 E87055	probable conserved
19	35	64.8	251	2 S72791	hypothetical prote
20	35	64.8	271	2 B83617	hypothetical prote
21	35	64.8	310	2 T19379	hypothetical prote
22	35	64.8	468	2 S70992	DNA topoisomerase
23	35	64.8	662	2 I36792	hypothetical prote
24	35	64.8	669	2 S46519	luciferin-binding
25	35	64.8	822	2 B98009	DNA topoisomerase
26	35	64.8	822	2 D95141	DNA gyrase chain A
27	35	64.8	822	2 T43720	DNA topoisomerase
28	35	64.8	829	2 G86763	DNA topoisomerase
29	35	64.8	829	2 T46556	DNA topoisomerase

30	35	64.8	830	2 G96900	DNA gyrase (topois
31	35	64.8	833	2 H81700	DNA gyrase, chain
32	35	64.8	834	2 B86525	DNA gyrase subunit
33	35	64.8	834	2 G72098	DNA gyrase chain A
34	35	64.8	834	2 F81571	DNA gyrase, chain
35	35	64.8	835	2 AH1861	DNA topoisomerase
36	35	64.8	836	2 F71546	probable DNA gyras
37	35	64.8	858	2 S30571	DNA topoisomerase
38	35	64.8	860	2 S76534	hypothetical prote
39	35	64.8	872	2 AB1914	DNA gyrase A chain
40	35	64.8	878	2 T43767	DNA topoisomerase
41	35	64.8	883	2 T03577	DNA topoisomerase
42	35	64.8	894	2 E82221	DNA gyrase, chain
43	35	64.8	902	2 AF3362	DNA topoisomerase
44	35	64.8	905	2 A97734	DNA topoisomerase
45	35	64.8	905	2 H71731	DNA gyrase chain A

ALIGNMENTS

RESULT 1

T18477
hypothetical protein C0485w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18477
R;Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z18937
A;Accession: T18477
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-2523 <LAW>
A;Cross-references: UNIPROT:O77365; UNIPARC:UPI000017CC31; EMBL:AL008970; NID:el407852;
C;Genetics:
A;Map position: 3
A;Introns: 148/3
A;Note: C0485w

Query Match 75.9%; Score 41; DB 2; Length 2523;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VSIPPRNLGY 10
|.:|:|:|
Db 2263 VHVPNNIGY 2272

RESULT 2

T38885
probable ATP-dependent DNA helicase (EC 3.6.1.1-) - fission yeast (Schizosaccharomyces po
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38885
R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z21807
A;Accession: T38885
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-887 <MUR>
A;Cross-references: UNIPROT:Q10213; UNIPARC:UPI000013A195; EMBL:Z69380; PIDN:CAA93344.1;
A;Experimental source: strain 972h-; cosmid c4H3
C;Genetics:
A;Gene: SPDB:SPAC4H3.05
A;Map position: 1
A;Introns: 121/2; 209/3; 353/2
C;Keywords: hydrolase

Query Match 74.1%; Score 40; DB 2; Length 887;
Best Local Similarity 55.6%; Pred. No. 23;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 VSIPPRNLG 9
Db      431 INVPPRNIG 439

RESULT 3
AB3633
Nirv precursor [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AB3633
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A:Reference number: AD3252; PMID:11756688
A:Accession: AB3633
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-283 <KUR>
A:CROSS-references: UNIPROT:Q8YBB3; UNIPARC:UPI00000586C8; GB:AE008918; PIDN:AAL54229.1;
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME110987
A:Map position: 11

Query Match      70.4%; Score 38; DB 2; Length 283;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 VSIPPRNLG 10
Db      253 VGVPDPNLGF 262

RESULT 4
A99192
Nirv precursor (AF040987) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: A99192
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; PMID:21608551; PMID:11743194
A:Accession: A99192
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-315 <KUR>
A:CROSS-references: UNIPROT:Q8U7R8; UNIPARC:UPI00000D254E; GB:AE007870; PIDN:AAK89059.1;
C:Genetics:
A:Gene: AGR_L_972
A:Map position: linear chromosome

Query Match      70.4%; Score 38; DB 2; Length 315;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 VSIPPRNLG 10
Db      283 VGVPDPNLGF 292

RESULT 5
AI3094
Nitrite reductase, Nirv precursor [imported] - Agrobacterium tumefaciens (strain C58, Du
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AI3094
R:Wood, D.W.; Stetubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell

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; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AI3094
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-315 <KUR>
A:CROSS-references: UNIPROT:Q8U7R8; UNIPARC:UPI00000D254E; GB:AE008689; PIDN:AAL45175.1;
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: nirv
A:Map position: linear chromosome

Query Match      70.4%; Score 38; DB 2; Length 315;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 VSIPPRNLG 10
Db      283 VGVPDPNLGF 292

RESULT 6
D90086
DNA gyrase A-subunit [imported] - Guillardia theta nucleomorph
C:Species: nucleomorph Guillardia theta
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 05-Oct-2004
C:Accession: D90086
R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reit
Nature 410, 1091-1096, 2001
A:Title: The highly reduced genome of an enslaved algal nucleus.
A:Reference number: A99082; MUID:11323671; PMID:11323671
A:Accession: D90086
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-877 <DOU>
A:CROSS-references: UNIPROT:Q98RX7; UNIPARC:UPI000008C0E5; GB:AF165818; NID:gl3794448; P
C:Genetics:
A:Gene: gyra
A:Map position: 1
A:Genome: nucleomorph
C:Superfamily: Type II topoisomerase, subunit A; phage T4 DNA topoisomerase (ATP-hydroly
C:Keywords: nucleomorph

Query Match      70.4%; Score 38; DB 2; Length 877;
Best Local Similarity 87.5%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 SIPPRNLG 9
Db      239 SIPPRNLG 246

RESULT 7
S75188
Nirv topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) chain A - Synechocystis sp. (strain PC
N:Alternate names: DNA gyrase; protein ell1941
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 05-Oct-2004
C:Accession: S75188
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S75188
A>Status: nucleic acid sequence not shown; translation not shown

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 10, 2006, 19:13:10 ; Search time 381.064 Seconds
(without alignments)
740.245 Million cell updates/sec

Title: US-09-581-651D-2
Perfect score: 3687
Sequence: 1 MLRGPFGLLLVQLGTA.....ISKYILWRPVSTPPRNLGY 642

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3687	100.0	660	2	AAY28901 Human mig
2	3680	99.8	642	8	ADR67316 Human bla
3	3680	99.8	642	8	ADSL7489 Amino aci
4	3680	99.8	642	8	ADR97658 Human fib
5	3680	99.8	642	9	ADM44480 Human fib
6	3680	99.8	642	9	ADY55704 Human fib
7	3680	99.8	642	9	ADY32458 Human fib
8	3680	99.8	642	9	ADY32458 Event seq
9	3680	99.8	642	9	ADY32458 Event seq
10	3664	99.4	642	8	ADQ39403 Human fib
11	3653.5	99.1	657	9	ADZ26739 Human fib
12	3646.5	98.9	657	9	ADQ39409 Human myo
13	3599.5	97.6	2176	9	ADZ26741 Human fib
14	3599.5	97.6	2182	8	ADR66462 Human pro
15	3599.5	97.6	2182	8	ADZ26749 Human fib
16	3599.5	97.6	2220	6	ABO01289 Human pro
17	3599.5	97.6	2286	6	ABR40124 Human cel
18	3599.5	97.6	2236	9	ADZ26745 Human fib
19	3599.5	97.6	2330	9	ADZ26749 Human fib
20	3599.5	97.6	2355	6	ABR58335 NM_00202
21	3599.5	97.6	2355	7	ADP65196 Human fib
22	3599.5	97.6	2355	8	ADG9560 Human fib
23	3599.5	97.6	2355	8	ADO55175 Protein #
24	3599.5	97.6	2355	8	ADQ26085 Fibronect

25	3599.5	97.6	2355	8	ADQ29668 Human col
26	3599.5	97.6	2355	8	ADR67315 Human bla
27	3599.5	97.6	2355	9	ADV70223 Tumor-ase
28	3599.5	97.6	2355	9	ADZ26565 Human fib
29	3599.5	97.6	2355	9	AEA04490 Human pro
30	3599.5	97.6	2355	9	AEI17606 Human fib
31	3599.5	97.6	2355	9	AEBA7084 Human fib
32	3599.5	97.6	2386	8	ADO55174 Protein #
33	3599.5	97.6	2386	8	ADU24084 Human thr
34	3599.5	97.6	2421	9	ADZ26743 Human fib
35	3595.5	97.5	2386	5	AAO17353 Human fib
36	3595.5	97.5	2386	6	ABR81866 Human fib
37	3595.5	97.5	2386	7	ADD18770 Human dis
38	3595.5	97.5	2386	7	ADE63324 Human pro
39	3595.5	97.5	2386	8	ADR99200 Fibronect
40	3595.5	97.5	2386	9	ADM63879 Human fib
41	3595.5	97.5	2386	9	ADX57710 Rheumatoi
42	3595.5	97.5	2386	9	ADX69339 Human hep
43	3595.5	97.5	2386	9	ADZ36436 Human fib
44	3594.5	97.5	2476	9	ADZ26747 Human fib
45	3593.5	97.5	2446	3	AAB50377 Human fib

ALIGNMENTS

RESULT 1
AAY28901
ID AAY28901 standard; protein; 660 AA.
XX
AC AAY28901;
XX
DT 21-SEP-1999 (first entry)
XX
DE Human migration stimulating factor (MSF) 1-alpha protein.
XX
KW Migration stimulatory factor; MSF; cell migration; modulation; human;
wound healing; scarring; MSF1-alpha.
XX
OS Homo sapiens.
XX
PN WO9931233-A1.
XX
PD 24-JUN-1999.
XX
PF 15-DEC-1998; 98MO-GB003766.
XX
PR 16-DEC-1997; 97GB-00026539.
XX
(UYDU-) UNIV DUNDEE.
XX
PI Schor SL, Schor AM;
XX
DR WPI; 1999-430039/36.
XX
N-PSDB; AAX81299.
XX
PT Proteins with cell migration stimulatory activity used in treating wound
and preventing scarring.
XX
PS Claim 1; Page 53; 86pp; English.
XX
CC The invention provides a human migration stimulatory factor (MSF)
protein. Host cells containing a replicable vector comprising the MSF
encoding nucleic acid can be used for the recombinant production of the
protein. The polypeptide can be used for modulating cell migration,
healing a wound and for preventing scarring. The present sequence
represents the human MSF1-alpha protein
XX
SQ Sequence 660 AA;

Query Match 100.0%; Score 3687; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 1.4e-235;
Matches 642; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRGPGLLLAVQCLGTAVPSTGASKSKRQAOQWVQSPVAVSQSPGCGYDNGKHQ 60
 DB 19 MLRGPGLLLAVQCLGTAVPSTGASKSKRQAOQWVQSPVAVSQSPGCGYDNGKHQ 78
 QY 61 INQWERTYLGALVCTCYGSGRGFNCSKPEAEETCFDKYTGNTYRVGDTYERPKDSMI 120
 DB 79 INQWERTYLGALVCTCYGSGRGFNCSKPEAEETCFDKYTGNTYRVGDTYERPKDSMI 138
 QY 121 WDCTCTGAGRGISCTIANRCHGGOSYKIGDTRWRPHEGTGGYMLSCVCLGNGKGWTK 180
 DB 139 WDCTCTGAGRGISCTIANRCHGGOSYKIGDTRWRPHEGTGGYMLSCVCLGNGKGWTK 198
 QY 181 PIAEKCFDHAAGTSYVVGTEWEPYQGMWMDCTCLGEGSGRITCTSRNRCNDQDTRTSY 240
 DB 199 PIAEKCFDHAAGTSYVVGTEWEPYQGMWMDCTCLGEGSGRITCTSRNRCNDQDTRTSY 258
 QY 241 RIGDTSKKNRGNLLQICITGNRGWKCERHTSVQTTSSGSGPFTDVRAAYVQPPHP 300
 DB 259 RIGDTSKKNRGNLLQICITGNRGWKCERHTSVQTTSSGSGPFTDVRAAYVQPPHP 318
 QY 301 QPPYGHCVTDGSGVYVSGMQLKTOGNKQMLCTCLGNGVSCQETAVTQTYGNSGEP 360
 DB 319 QPPYGHCVTDGSGVYVSGMQLKTOGNKQMLCTCLGNGVSCQETAVTQTYGNSGEP 378
 QY 361 VLPFTYNDRTDSTTSNYEQDKYSFCTDHTVLVQTRGNSNGALCHFPFLYNNHYTDCT 420
 DB 379 VLPFTYNDRTDSTTSNYEQDKYSFCTDHTVLVQTRGNSNGALCHFPFLYNNHYTDCT 438
 QY 421 SEGRDNMKWCGTQNYDADQKFGFCPMAAHEICTTNEGVMYRIGDQWDKQHDGMHMR 480
 DB 439 SEGRDNMKWCGTQNYDADQKFGFCPMAAHEICTTNEGVMYRIGDQWDKQHDGMHMR 498
 QY 481 CTCVNGRGWTCIAYSQRLDQCIYDDITVYNDTFHKRHEGHMLNCTCFGGGRWKC 540
 DB 499 CTCVNGRGWTCIAYSQRLDQCIYDDITVYNDTFHKRHEGHMLNCTCFGGGRWKC 558
 QY 541 DPVDCQDSETGTFYQIGDSWEKYVHGVRQCYCGRGIGEWHCQPLQTYPSSSGPVEVF 600
 DB 559 DPVDCQDSETGTFYQIGDSWEKYVHGVRQCYCGRGIGEWHCQPLQTYPSSSGPVEVF 618
 QY 601 ITETPSQNSHPIQWNAPOPSHISKYLRLWRPVSIPPRNLGY 642
 DB 619 ITETPSQNSHPIQWNAPOPSHISKYLRLWRPVSIPPRNLGY 660

RESULT 2

ADR67316
 ID ADR67316 standard; protein; 642 AA.

AC ADR67316;

DT 02-DEC-2004 (first entry)

DE Human bladder cancer associated amino acid sequence.

KW bladder cancer tissue; bladder cancer; cytostatic.

XX Homo sapiens.

PN WO2004076613-A2.

XX 10-SEP-2004.

XX 24-FEB-2004; 2004WO-DE000364.

XX 26-FEB-2003; 2003DE-01009729.

XX (HERR/) HERR A.

PA (HINZ/) HINZMANN B.

PA (DAHL/) DAHL E.

PA (STAUG/) STAUB E.

PA (PILA/) PILARSKY C.

(SPEC/) SPECHT T.

XX Herr A, Hinzmann B, Dahl E, Staub E, Pilarsky C, Specht T;

XX WPI; 2004-653385/63.

XX New nucleic acids, and encoded proteins, from bladder cancer tissue,
 PT useful for diagnosis, treatment and in screening for specific binding
 PT agents.

XX Claim 2; Fig 3; 112pp; German.

XX The present invention describes nucleic acids (I) associated with bladder
 CC cancer tissue. Also described: (1) peptides and proteins (II) containing
 CC an amino acid sequence encoded by (I); (2) a method for diagnosing
 CC bladder cancer (BC), or monitoring its progression, that uses (I), (II)
 CC or agents (Z) that inhibit, or bind to, (I) or (II), labelled with a
 CC reporter; and (3) a method for treating BC that uses (I), (II) or (Z).
 CC (I) and (II) have cytostatic activity. (I) and (II) can be used to detect
 CC (and monitor progression of) bladder cancer (BC), or the risk of
 CC developing it; to screen for specific binding agents (Z), and to treat
 CC BC. (Z) are also useful as diagnostic and therapeutic agents. The present
 CC sequence represents a human amino acid sequence associated with bladder
 CC cancer, which is used in the exemplification of the present invention.

XX Sequence 642 AA;

Query Match 99.8%; Score 3680; DB 8; Length 642;

Best Local Similarity 99.8%; Pred. No. 3.8e-235;

Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLRGPGLLLAVQCLGTAVPSTGASKSKRQAOQWVQSPVAVSQSPGCGYDNGKHQ 60

DB 1 MLRGPGLLLAVQCLGTAVPSTGASKSKRQAOQWVQSPVAVSQSPGCGYDNGKHQ 60

QY 61 INQWERTYLGALVCTCYGSGRGFNCSKPEAEETCFDKYTGNTYRVGDTYERPKDSMI 120

DB 61 INQWERTYLGALVCTCYGSGRGFNCSKPEAEETCFDKYTGNTYRVGDTYERPKDSMI 120

QY 121 WDCTCTGAGRGISCTIANRCHGGOSYKIGDTRWRPHEGTGGYMLSCVCLGNGKGWTK 180

DB 121 WDCTCTGAGRGISCTIANRCHGGOSYKIGDTRWRPHEGTGGYMLSCVCLGNGKGWTK 180

QY 181 PIAEKCFDHAAGTSYVVGTEWEPYQGMWMDCTCLGEGSGRITCTSRNRCNDQDTRTSY 240

DB 181 PIAEKCFDHAAGTSYVVGTEWEPYQGMWMDCTCLGEGSGRITCTSRNRCNDQDTRTSY 240

QY 241 RIGDTSKKNRGNLLQICITGNRGWKCERHTSVQTTSSGSGPFTDVRAAYVQPPHP 300

DB 241 RIGDTSKKNRGNLLQICITGNRGWKCERHTSVQTTSSGSGPFTDVRAAYVQPPHP 300

QY 301 QPPYGHCVTDGSGVYVSGMQLKTOGNKQMLCTCLGNGVSCQETAVTQTYGNSGEP 360

DB 301 QPPYGHCVTDGSGVYVSGMQLKTOGNKQMLCTCLGNGVSCQETAVTQTYGNSGEP 360

QY 361 VLPFTYNDRTDSTTSNYEQDKYSFCTDHTVLVQTRGNSNGALCHFPFLYNNHYTDCT 420

DB 361 VLPFTYNDRTDSTTSNYEQDKYSFCTDHTVLVQTRGNSNGALCHFPFLYNNHYTDCT 420

QY 421 SEGRDNMKWCGTQNYDADQKFGFCPMAAHEICTTNEGVMYRIGDQWDKQHDGMHMR 480

DB 421 SEGRDNMKWCGTQNYDADQKFGFCPMAAHEICTTNEGVMYRIGDQWDKQHDGMHMR 480

QY 481 CTCVNGRGWTCIAYSQRLDQCIYDDITVYNDTFHKRHEGHMLNCTCFGGGRWKC 540

DB 481 CTCVNGRGWTCIAYSQRLDQCIYDDITVYNDTFHKRHEGHMLNCTCFGGGRWKC 540

QY 541 DPVDCQDSETGTFYQIGDSWEKYVHGVRQCYCGRGIGEWHCQPLQTYPSSSGPVEVF 600

DB 541 DPVDCQDSETGTFYQIGDSWEKYVHGVRQCYCGRGIGEWHCQPLQTYPSSSGPVEVF 600

QY 601 ITETPSQNSHPIQWNAPOPSHISKYLRLWRPVSIPPRNLGY 642

|||||

GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 12, 2006, 11:45:28 ; Search time 4776.6 Seconds
(without alignments)
822.262 Million cell updates/sec

Title: US-09-581-651d-2

Perfect score: 3687

Sequence: 1 MLRGPGLLLAVQCLGTA.....ISKYLWRPVSIPPRNLGY 642

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9312410 seqs, 2039259788 residues

Total number of hits satisfying chosen parameters: 18624820

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Published Applications NA New:
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2: /SID55/ptodata/2/pubpna/US06 NEW PUB.seq.*
3: /SID55/ptodata/2/pubpna/US07 NEW PUB.seq.*
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19: /SID55/ptodata/2/pubpna/US11 NEW PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

* *

Alignment Scores:

Pred. No.:

5.07e-281

Length:

2443

No.	Score	Match	Length	DB	ID	Description
1	3658	99.2	2443	10	US-10-995-561-114	Sequence 114, App
2	3653.5	99.1	2402	17	US-11-193-561-26	Sequence 26, Appl
3	3653.5	99.1	2402	17	US-11-193-771-26	Sequence 26, Appl
4	3653.5	99.1	2402	17	US-11-193-789-26	Sequence 26, Appl
5	3653.5	99.1	2402	17	US-11-193-806-26	Sequence 26, Appl
6	3653.5	99.1	2402	17	US-11-193-857-26	Sequence 26, Appl
7	3640.5	98.7	2488	10	US-10-995-561-105	Sequence 105, App
8	3599.5	97.6	7912	17	US-11-193-561-24	Sequence 24, Appl
9	3599.5	97.6	7912	17	US-11-193-771-24	Sequence 24, Appl
10	3599.5	97.6	7912	17	US-11-193-789-24	Sequence 24, Appl
11	3599.5	97.6	7912	17	US-11-193-806-24	Sequence 24, Appl
12	3599.5	97.6	7912	17	US-11-193-857-24	Sequence 24, Appl
13	3599.5	97.6	8232	10	US-10-821-234-693	Sequence 693, App
14	3599.5	97.6	8272	17	US-11-193-561-22	Sequence 22, Appl
15	3599.5	97.6	8272	17	US-11-193-771-22	Sequence 22, Appl
16	3599.5	97.6	8272	17	US-11-193-789-22	Sequence 22, Appl
17	3599.5	97.6	8272	17	US-11-193-806-22	Sequence 22, Appl
18	3599.5	97.6	8272	17	US-11-193-857-22	Sequence 22, Appl
19	3599.5	97.6	8374	17	US-11-193-561-20	Sequence 20, Appl
20	3599.5	97.6	8374	17	US-11-193-771-20	Sequence 20, Appl
21	3599.5	97.6	8374	17	US-11-193-789-20	Sequence 20, Appl
22	3599.5	97.6	8374	17	US-11-193-806-20	Sequence 20, Appl
23	3599.5	97.6	8374	17	US-11-193-857-20	Sequence 20, Appl
24	3599.5	97.6	8449	17	US-11-193-561-18	Sequence 18, Appl
25	3599.5	97.6	8449	17	US-11-193-771-18	Sequence 18, Appl
26	3599.5	97.6	8449	17	US-11-193-789-18	Sequence 18, Appl
27	3599.5	97.6	8449	17	US-11-193-806-18	Sequence 18, Appl
28	3599.5	97.6	8449	17	US-11-193-857-18	Sequence 18, Appl
29	3599.5	97.6	8647	17	US-11-193-561-16	Sequence 16, Appl
30	3599.5	97.6	8647	17	US-11-193-771-16	Sequence 16, Appl
31	3599.5	97.6	8647	17	US-11-193-789-16	Sequence 16, Appl
32	3599.5	97.6	8647	17	US-11-193-806-16	Sequence 16, Appl
33	3599.5	97.6	8647	17	US-11-193-857-16	Sequence 16, Appl
34	3599.5	97.6	8815	17	US-11-193-561-14	Sequence 14, Appl
35	3599.5	97.6	8815	17	US-11-193-771-14	Sequence 14, Appl
36	3599.5	97.6	8815	17	US-11-193-789-14	Sequence 14, Appl
37	3599.5	97.6	8815	17	US-11-193-806-14	Sequence 14, Appl
38	3599.5	97.6	8815	17	US-11-193-857-14	Sequence 14, Appl
39	3586.5	97.3	6510	10	US-10-995-561-112	Sequence 112, App
40	3586.5	97.3	7823	10	US-10-995-561-117	Sequence 117, App
41	3586.5	97.3	7848	10	US-10-995-561-111	Sequence 111, App
42	3586.5	97.3	7935	10	US-10-995-561-113	Sequence 113, App
43	3586.5	97.3	7959	10	US-10-995-561-108	Sequence 108, App
44	3586.5	97.3	8013	10	US-10-995-561-104	Sequence 104, App
45	3586.5	97.3	8155	10	US-10-995-561-116	Sequence 116, App

ALIGNMENTS

RESULT 1

US-10-995-561-114
; Sequence 114, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: C0001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 2443
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-114

Result

Score:	3658.00	Matches:	638
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Best Local Similarity:	99.4%	Mismatches:	4
Query Match:	99.2%	Indels:	0
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DB	373	ATGCTTAGGGGTCGGGGCCGGGCTGCTGCTGGCCGTCGTCGTCGGGACAGCG	432
QY	21	ValProSerThrGlyAlaSerLysSerLysArgGlnAlaGlnMetValGlnProGln	40
DB	433	GTGCCCTCCACGGGAGCTCGAAGACGACAGGCGCTCAGCAATGGTTGACGCCCG	492
QY	41	SerProValAlaValSerGlnSerLysProGlyCysTyrAspAsnGlyLysHisTyrGln	60
DB	493	TCCCGGTGGCTGTCAGTCAAGCAAGCCGGTGTATTGACAAATGGMAAACACTATCAG	552
QY	61	IleAsnGlnGlnTrpGluArgThrTyrLeuGlyAsnAlaLeuValCysThrCysTyrGly	80
DB	553	ATAAATCAACAGTGGGAGCGGACCTACCTAGGCAATGCGTTGGTTGTACTTGTATGGA	612
QY	81	GlySerArgGlyPheAsnCysGluSerLysProGluAlaGluGluThrCysPheAspLys	100
DB	613	GGAAGCGAGTTTAACTCGAGAGTAACCTGAAAGCTGAAAGACTTGTCTTGACAAAG	672
QY	101	TyrThrGlyAsnThrTyrArgValGlyAspThrTyrGluArgProLysAspSerMetile	120
DB	673	TACACTGGGAACACTTACCAGTGGGTGACACTTATGAGCGTCTTAAAGACTCCATGATC	732
QY	121	TrpAspCysThrCysIleGlyAlaGlyArgGlyArgIleSerCysThrIleAlaAsnArg	140
DB	733	TGGGACTGTACCTACCTACAGATTGGTGACACCTGGAGGAGACCAATGAGACT	792
QY	141	CysHisGluGlyGlnSerTyrLysIleGlyAspThrTyrArgArgProHisGluThr	160
DB	793	TGCCATGAAGGGGTGACTCTACAGATTGGTGACACCTGGAGGAGACCAATGAGACT	852
QY	161	GlyGlyTyrMetLeuGluCysValCysLeuGlyAsnGlyLysGlyGluTrpThrCysLys	180
DB	853	GGTGGTTACATGTTAGAGTGTGTGTCTTGGTAATGGMAAAGAGATGGACCTGCAAG	912
QY	181	ProIleAlaGlnLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr	200
DB	913	CCCATAGCTGAGAAGTGTGTGATCATGCTGCTGGGACTTCTTATGTGTCGAGAAACG	972
QY	201	TrpGluLysProTyrGlnGlyTyrMetMetValAspCysThrCysLeuGlyGlySer	220
DB	973	TGGGAGAGCCCTACCAAGCTGGATGATGGTAGATTGTACTTGGCTGGGAGAGGACGC	1032
QY	221	GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr	240
DB	1033	GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACCAAGGACATCCTAT	1092
QY	241	ArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuGlnCysIleCys	260
DB	1093	AGAAATGGAGACACCTGGAGCAAGAGGATTAATCGAGGAACCTGCTCAGTGCATCTGC	1152
QY	261	ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer	280
DB	1153	ACAGGCNAAGCGCGAGGAGTGGNAGTGTGAGAGGCACACCTCTGTGACAGCACATCG	1212
QY	281	SerGlySerGlyProPheThrAspValArgAlaValTyrGlnProGlnProHisPro	300
DB	1213	AGCGGATCTGGCCCTTACCGGATGTTGTCGACGCTGTTTACCAACCGCAGCGCTCACCCG	1272
QY	301	GlnProProTyrGlyHisCysValThrAspSerGlyValValTyrSerValGlyMet	320
DB	1273	CAGCCTCCTCCCTATGGCCACTGTGTACAGACAGAGTGGTGGTGTACTCTGTGGGGATG	1332
QY	321	GlnTrpLeuLysThrGlnGlyAsnLysGlnMetLeuCysThrCysLeuGlyAsnGlyVal	340
DB	1333	CAGTGGCTGAAGACACACAGGAATAAGCAAAATGCTTTGACGCTGCTGGCAACGGAGTC	1392
QY	341	SerCysGlnGluThrAlaValThrGlnThrTyrGlyGlyAsnSerAsnGlyGluProCys	360
DB	1393	AGCTGCCAAGAGACAGCTGTAAACCCAGACTTACRGTTGGCACTCAAAATGGAGAGCCATGT	1452
QY	361	ValLeuProPheThrTyrAsnAspArgThrAspSerThrThrSerAsnTyrGluGlnAsp	380
DB	1453	GTCTTACCATTACCTTACCAATGGCAGGAGCTGCAGACCAACTTCGAATTTATGACAGGAC	1512
QY	381	GlnLysTyrSerPheCysThrAspHisThrValLeuValGlnThrArgGlyGlyAsnSer	400
DB	1513	CAGNAATACTCTTCTGCACACACACTGTTTGGTTTCAGACTCGAGGAGGAATTC	1572
QY	401	AsnGlyAlaLeuCysHisPheProPheLeuTyrAsnAsnHisAsnTyrThrAspCysThr	420
DB	1573	AATGGTGCCTTGGCCACTTCCCTTCTATCAACACCACTTATACACTGATTGCACT	1632
QY	421	SerGluGlyArgArgAspAsnMetLysTrpCysGlyThrThrGlnAsnTyrAspAlaAsp	440
DB	1633	TCTGAGGGCAGAGAGACCAACATGAAGTGGTGGGACCCACAGAACCTATGATGCCGAC	1692
QY	441	GlnLysPheGlyPheCysProMetAlaAlaHisGluGluIleCysThrThrAsnGluGly	460
DB	1693	CAGNAGTTTGGCTTCTGCCCATGGCTGCCACGAGGAATCTGCACACCACTTGAAGGG	1752
QY	461	ValMetTyrArgIleGlyAspGlnTrpAspLysGlnHisAspMetGlyHisMetMetArg	480
DB	1753	GTCACTGATCCGATTTGGAGATCAGTGGGATAAGCAGCATGACATGGGTGCATGATGAGG	1812
QY	481	CysThrCysValGlyAsnGlyArgGlyGluTrpThrCysIleAlaTyrSerGlnLeuArg	500
DB	1813	TGCAGTGTGTTGGGAATGGTCTGGGGAATGGACATGCTTCCCTTCTCGCAGCTTCGA	1872
QY	501	AspGlnCysIleValAspAspIleThrTyrAsnValAsnAspThrPheHisLysArgHis	520
DB	1873	GATCAGTGCAATTTGATGACATCATTTACAATGTGAACGACACATTCACAAGCGTCAT	1932
QY	521	GluGluGlyHisMetLeuAsnCysThrCysPheGlyGlnGlyArgGlyArgTrpLysCys	540
DB	1933	GAAGAGGGGCACATGCTGAACCTGTATCATGCTTCGGTCAAGGTCGGGGCAGGTGGAAGTGT	1992
QY	541	AspProValAspGlnCysGlnAspSerGluThrGlyThrPheTyrGlnIleGlyAspSer	560
DB	1993	GATCCCGTCGACCAATGCCAGGATTCAGAGACTGGACGCTTTTATCAAAATGGAGATTCA	2052
QY	561	TrpGluLysTyrValHisGlyValArgTyrGlnCysTyrCysTyrArgGlyIleGly	580
DB	2053	TGGGAGAGATGTGTCATGGTGCAGATACCACTGCTACTGCTATGGCCGTCGTCATTGGG	2112
QY	581	GluTrpHisCysGlnProLeuGlnThrTyrProSerSerSerGlyProValGluValPhe	600
DB	2113	GAGTGGCATTTGCCAACCTTTACAGACCTATCCAAAGCTCAAGTGGTCTCTCGAAGTATTT	2172
QY	601	IleThrGluThrProSerGlnProAsnSerHisProIleGlnTrpAsnAlaProGlnPro	620
DB	2173	ATCACTGAGACTCCGAGTCAGCCCACTCCCAACCCCATCCAGTGGAAATGCCACAGCCA	2232
QY	621	SerHisIleSerLysTyrIleLeuArgTrpArgProValSerIleProProArgAsnLeu	640
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QY	641	GlyTyr 642	
DB	2293	GGATAC 2298	

RESULT 2

US-11-193-561-26

; Sequence 26, Application US/11193561

; Publication NO. US20060024757A1

; GENERAL INFORMATION:

; APPLICANT: Hussa, Robert

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

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(without alignments)
5217.711 Million cell updates/sec

Title: US-09-581-651D-2

Perfect score: 3687

Sequence: 1 MLKGPGLLLAVQCLGTA.....ISKYILRWPRVSIIPRNLGY 642

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-O=/abs/ABSSWEB spool/US09581651/runat.10052006.181222.525/app.query.fasta_1
-DB=Published Applications_NA_Main -QWTF=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -MODE=LOCAL -OUTFMT=pto -NORM=ext
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-HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs03p
-USER=US09581651 @CGN 1.1 2064 @runat.10052006.181222.525 -NCPU=6 -ICPU=3
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA Main:

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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3671	99.6	2127	9	US-10-956-157-4288
2	3665	99.4	2443	7	US-10-741-601-70
3	3665	99.4	2443	8	US-10-741-600-238
4	3664	99.4	2127	6	US-10-210-120-49
5	3664	99.4	2127	9	US-10-909-035-49
6	3647.5	98.9	2488	7	US-10-741-601-75
7	3647.5	98.9	2488	8	US-10-741-600-244

8	3599.5	97.6	7361	7	US-10-236-392-3
9	3599.5	97.6	8027	7	US-10-447-161-8
10	3599.5	97.6	8027	7	US-10-734-564-27
11	3599.5	97.6	8027	9	US-10-852-335A-53
12	3599.5	97.6	8027	9	US-10-287-436A-81
13	3599.5	97.6	8815	8	US-10-868-577A-62
14	3599.5	97.6	8815	8	US-10-868-549-21
15	3599.5	97.5	6510	7	US-10-741-601-72
16	3593.5	97.5	6510	8	US-10-741-600-241
17	3593.5	97.5	7823	7	US-10-741-601-77
18	3593.5	97.5	7823	8	US-10-741-600-245
19	3593.5	97.5	7848	7	US-10-741-601-78
20	3593.5	97.5	7848	8	US-10-741-600-246
21	3593.5	97.5	7935	7	US-10-741-601-74
22	3593.5	97.5	7935	7	US-10-741-600-240
23	3593.5	97.5	7959	7	US-10-741-601-81
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25	3593.5	97.5	8013	7	US-10-741-601-71
26	3593.5	97.5	8013	8	US-10-741-600-242
27	3593.5	97.5	8155	7	US-10-741-601-79
28	3593.5	97.5	8155	8	US-10-741-600-247
29	3593.5	97.5	8226	7	US-10-741-601-69
30	3593.5	97.5	8226	8	US-10-741-600-237
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34	3593.5	97.5	8332	8	US-10-741-600-239
35	3593.5	97.5	8371	7	US-10-741-601-76
36	3593.5	97.5	8371	8	US-10-741-600-243
37	3592.5	97.4	7795	5	US-10-084-817-2
38	3592.5	97.4	7867	5	US-10-098-841-6
39	3592.5	97.4	8044	6	US-10-240-965-121
40	3592.5	97.4	8044	9	US-10-765-700-135
41	3592.5	97.4	8062	5	US-10-098-841-5
42	3592.5	97.4	8137	5	US-10-098-841-8
43	3592.5	97.4	8230	5	US-10-098-841-7
44	3524	95.6	4295	6	US-10-144-194A-51
45	3524	95.6	4295	8	US-10-491-566-51

ALIGNMENTS

RESULT 1

US-10-956-157-4288
; Sequence 4288, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4288
; LENGTH: 2127
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-956-157-4288

Alignment Scores:
Pred. No.: 0
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Percent Similarity: 99.7%
Best Local Similarity: 99.7%
Query Match: 99.6%
DB: 9
Length: 2127
Matches: 640
Conservative: 0
Mismatches: 2
Indels: 0
Gaps: 0

US-09-581-651D-2 (1-642) x US-10-956-157-4288 (1-2127)

Qy 1 MetLeuArgGlyProGlyLeuLeuLeuAlaValGlnCysLeuGlyThrAla 20

GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 12, 2006, 10:33:26 ; Search time 412.574 Seconds
(without alignments)
4149.058 Million cell updates/sec

Title: US-09-581-651D-2

Perfect score: 3687

Sequence: 1 MLRGPGLLLAVQCLGTA.....ISKVILWRVPSIPPNLGY 642

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSSWEB.spool/US09581651/runat_10052006_181213_253/app_query.fasta_1
-DB=Issued Patents NA -OPMT=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosun62 -TRANS=human40.cdi
-LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abs04 -USER=US09581651 @CGN 1 1 237 @runat_10052006_181213_253 -NCPU=6
-ICPU=3 -NO MAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

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4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
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8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3592.5	97.4	8044	3	US-09-566-921-135
2	3578.5	97.1	7803	2	Sequence 135, App
3	3578.5	97.1	7803	6	Sequence 1, Appli
4	3448.5	93.5	7679	3	PCT-US93-12687-1
5	3448.5	93.5	7680	3	US-09-220-132-38
6	3448.5	93.5	7680	6	US-09-023-655-1289
7	3433.5	93.1	7705	2	PCT-US95-09819-6
8	3433.5	93.1	7705	2	US-08-259-569-16
9	3428.5	93.0	7705	9	US-08-826-885-16
					Patent No. 5455158-2

10	1665.5	45.2	986	2	US-07-637-250A-8	Sequence 8, Appli
11	1665.5	45.2	986	2	US-08-145-061-8	Sequence 8, Appli
12	325.5	8.8	2109	3	US-09-799-451-345	Sequence 345, App
13	311	8.4	2335	3	US-09-799-451-346	Sequence 346, App
14	306.5	8.3	2333	2	US-08-392-678-33	Sequence 33, Appl
15	305.5	8.3	2334	2	US-08-457-304A-33	Sequence 33, Appl
16	305.5	8.3	2334	2	US-08-456-701A-33	Sequence 33, Appl
17	305.5	8.3	2334	3	US-08-684-932A-33	Sequence 33, Appl
18	305.5	8.3	2334	3	US-09-023-655-996	Sequence 996, App
19	305.5	8.3	2334	3	US-09-949-016-704	Sequence 704, App
20	305.5	8.3	2335	3	US-09-949-016-4758	Sequence 4758, Ap
21	302	8.2	1983	3	US-09-949-016-2066	Sequence 2066, Ap
22	302	8.2	3059	3	US-09-949-016-641	Sequence 641, App
23	298	8.1	2123	3	US-09-194-468A-29	Sequence 29, Appl
24	294.5	8.0	567	2	US-08-142-449B-5	Sequence 5, Appli
25	225	6.1	11665	3	US-09-949-016-12446	Sequence 12446, A
26	225	6.1	11665	3	US-09-949-016-16500	Sequence 16500, A
27	217.5	5.9	4588	3	US-08-840-062-1	Sequence 1, Appli
28	208	5.6	4627	3	US-09-949-016-935	Sequence 935, App
29	208	5.6	5633	3	US-09-023-655-1490	Sequence 1490, Ap
30	199.5	5.4	4892	3	US-09-976-594-167	Sequence 167, App
31	199.5	5.4	5158	3	US-09-023-655-1347	Sequence 1347, Ap
32	197	5.3	4621	3	US-09-949-016-4577	Sequence 4577, Ap
33	197	5.3	5627	3	US-09-949-016-2444	Sequence 2444, Ap
34	196.5	5.3	29954	3	US-09-949-016-13808	Sequence 13808, A
35	196.5	5.3	31040	3	US-09-949-016-12383	Sequence 12383, A
36	193.5	5.2	4464	2	US-08-400-159-7	Sequence 7, Appli
37	193.5	5.2	4483	3	US-08-611-729A-7	Sequence 7, Appli
38	193.5	5.2	4483	3	US-09-195-524-7	Sequence 7, Appli
39	193.5	5.2	4483	3	US-09-310-685-5	Sequence 5, Appli
40	193	5.2	3955	3	US-09-214-278-4	Sequence 4, Appli
41	193	5.2	3955	3	US-09-855-722-4	Sequence 3, Appli
42	189.5	5.1	4771	3	US-08-840-062-3	Sequence 30388, A
43	189	5.1	601	3	US-09-949-016-30391	Sequence 30391, A
44	189	5.1	601	3	US-09-949-016-70162	Sequence 70162, A
45	189	5.1	601	3		

ALIGNMENTS

RESULT 1

US-09-566-921-135
; Sequence 135, Application US/09566921
; Patent No. 668288
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 135
; LENGTH: 8044
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 427813.14
US-09-566-921-135

Alignment Scores:
Pred. No.: 5 87e-312 Length: 8044
Score: 3592.50 Matches: 629
Percent Similarity: 97.2% Conservative: 0
Best Local Similarity: 97.2% Mismatches: 3
Query Match: 97.4% Indels: 15
DB: 3 Gaps: 1

US-09-581-651D-2 (1-642) x US-09-566-921-135 (1-8044)

GenCore version 5.1.18
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 12, 2006, 10:25:20 ; Search time 9261.74 Seconds
(without alignments)
4864.742 Million cell updates/sec

Title: US-09-581-651D-2
Perfect score: 3687
Sequence: 1 MLRCPGGLLLAVQCLGTA.....ISKYLWRPVSIPPNLGY 642

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs03h
-USER=US09581651 @CGN 1.1 6731 @runat 10052006 181209 176 -ICPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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3: gb_est3.*
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5: gb_est5.*
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7: gb_est7.*
8: gb_est8.*
9: gb_est9.*
10: gb_est10.*
11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Length	ID	Description
1	3592.5	97.4	7868	4 HSM806653 BX640608 Homo sapi
2	3592.5	97.4	8411	4 HSM806992 BX640875 Homo sapi
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4	3588.5	97.3	7777	4 CR749316 CR749317 Homo sapi
5	3567.5	96.8	8121	4 CR749317 CR749317 Homo sapi
6	3564.5	96.7	7501	4 BC078656 Homo sapi
7	3564.5	96.7	7501	4 BC100030 Homo sapi

8	3389.5	91.9	8315	4 AK090135
9	3278	88.9	8329	4 AK090130
10	2485.5	67.4	7434	11 DQ039102
11	1804.5	48.9	7434	11 DQ039103
C 12	1573.5	42.7	943	5 BX391752
C 13	1564	42.4	1044	5 BX398837
14	1496	40.6	2107	4 AK054456
15	1450.5	40.4	836	7 CNS38822
C 16	1480	40.1	1052	5 BX380582
17	1478	40.1	816	1 AU141008
18	1464	39.7	859	6 CF616056
19	1460	39.6	766	7 CN419594
20	1451.5	39.4	861	1 AU140971
21	1419.5	38.5	785	3 CN534124
22	1415	38.4	761	3 BM715855
23	1400	38.0	808	7 CK638401
24	1390	37.7	837	1 AU140973
25	1386	37.6	731	1 AU140526
26	1381	37.5	737	1 AU140993
27	1369	37.1	959	5 BU109952
28	1356	36.8	739	1 AL706215
29	1356	36.8	1026	5 BX386270
30	1351	36.6	695	7 CN419477
31	1349	36.6	729	1 AU140834
32	1342	36.4	849	8 DR835543
33	1340	36.3	772	7 CN530412
34	1336	36.2	799	8 CX899584
35	1329.5	36.1	781	7 CN161442
36	1323	35.9	699	1 AU140889
37	1309.5	35.5	856	8 CX894723
38	1308.5	35.5	1050	5 BX417945
39	1308	35.5	723	7 CN419622
C 40	1304.5	35.4	780	7 CN162843
41	1303	35.3	738	6 CD613781
42	1302.5	35.3	748	1 AU140948
43	1299	35.2	829	8 CX901794
44	1298	35.2	667	1 AU140910
45	1295.5	35.1	796	1 AU140814

ALIGNMENTS

RESULT 1
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LOCUS Homo sapiens mRNA; cDNA DKFp686M04163 (from clone DKFp686M04163). linear 7868 bp mRNA
DEFINITION Homo sapiens mRNA; cDNA DKFp686M04163 (from clone DKFp686M04163). linear 7868 bp mRNA
ACCESSION BX640608
VERSION BX640608.1 GI:34364616
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (bases 1 to 7868)
Boecker,H., Boecker,M., Brandt,P., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
The German cDNA Consortium
Direct Submission
Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
COMMENT
This clone (DKFp686M04163) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFp686M04163
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers

FEATURES


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QSLLISTQTADAPDPPTVDQVDTSIYVRMSRPOALITGRIVTSVEGSGSTEL
NLPTANSYTLSDIQGVQNNIILYAEVNEQSPVVIQETTTPRSVTVPSPRLQ
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VGLTRRQOPQYVNGPSVSKPLRNLQAPASRYTSLVAIKGNOESPATGVFTTLOPG
SSIIPYNETVETTTIVITWTPAPRIGPKLVRSQSGEAPREVTSGSIYVSGSLPG
VEYVYITQVLRDQERDAPLVNKVWPLSPETNLHLAEANPDGTGLVTSWERSSTPOLI
GYRITITPTNGQQNSLEEVHADQSSCTFDNLSPGLEYNVSYTTVKDKRSTPISDI
IIPAVPTPLDLRFYINIGDTRVMTWAPPSIDLTNFLVRSYVKNBEDEVAELSI5PSD
NAVYLTLDFTFYVNSVSVSYEQHSETPLRGKQLDLSPTGDSITANSTFTVHM
IAPRATTYGYRIHRHPEHFRPREDRVPHRSNITUTNLTPTGYEYVGSIVALNGREE
SPILLIQGQSTVYVRODLEVAATPTSLILSWDAPAVTRYRYITVGETGNSPVQEF
TVPGSKSTATISGLPKGVDTIIVYATVGRGDSPASSKPIINRYTEIDKPSQOMQYD
VQGNSISVKWLPSSSPVGYRVTTPKNGPGTKTKTAPDQTEMIEGLQPTVEYVY
SVYANQSPSGESQLQVATVITIPATDLKFTQVPTLSLAQWTPPNVGRVTRVTP
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PRARVATDATTETITISWRTKTTITGFQDAPVANGQTPIQRTIKPDVRSYITGLQ
PGDTKYLYLTANDNARSPVVIADTAIDANSLRELAITPNLSLVWSQPPRARIY
YIKYKXPGSPPREVPRPGVTAEATITGLEPTEYTIIVIALKKNKSEPELIGRKY
TDELPOLVTLPHNLHGTEILDVPSVTOKTPFVTHPGYDTNGIQLPSTSGQSPSVQ
QMIPFEHGFRTPPTPTATPIRHPRPYPNVGEEIQIHIPREDVDYHLYPHGPGLN
PNASTGQSQTTISWAPDQSTSEYIISCHPVGTDEEPLQFRVPGTSTATLITGLR
GATYNIIVALKQQRHKHREVVTVGNSVGNLNPQTDSDCFDPTVSHVAYGDWE
RMSBSGPKLQCLQGHGFRCDNRSHWDGNGVNYKIGEKWDQSGENGQMSCTCLG
NGKGEPCDHEATCYDDGKTYHGEQWKEYLGAICSTCFGQGRGVCDNCRRPGR
EPTPEGITGGSYNOYSRHORYTNVNCPIECFMAIDVQADRESRRE"

```

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity: 97.28

Length: 7868

Matches: 629

Conservative: 0

Mismatches: 3

GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 12, 2006, 09:52:22 ; Search time 1039.8 Seconds
(without alignment)

6172.414 Million cell updates/sec

Title: US-09-581-651D-2

Perfect score: 3687

Sequence: 1 MLRPGFGGULLLAQCGLTA.....ISKYILWRPVSIPRNLGY 642

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=N Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs03p
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Database :

N Geneseq 21.*

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11: Geneseqn2003ds.*
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13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	3687	100.0	2147	2 AAX81299	Aax81299 Human mig
2	3680	99.8	1929	13 ADL17488	Adsl17488 Nucleotid
3	3680	99.8	1929	13 AD97657	Adr97657 Human fib
4	3680	99.8	1929	14 ADW4479	Adw44479 Human fib

ALIGNMENTS

RESULT 1
AAX81299

ID AAX81299 standard; cDNA; 2147 BP.

XX

AC AAX81299;

XX

DT 21-SBP-1999 (first entry)

XX

DE Human migration stimulating factor (MSF) 1-alpha encoding cDNA.

XX

KW Migration stimulatory factor; MSF; cell migration; modulation; human;

XX wound healing; scarring; MSF1-alpha; ss.

XX Homo sapiens.

XX

FN WO9931233-A1.

XX

PD 24-JUN-1999.

XX

PF 15-DEC-1998; 98WO-GB003766.

XX

PR 16-DEC-1997; 97GB-00026539.

XX

PA (UYDU-) UNIV DUNDEE.

XX

PI Schor SL, Schor AM;

XX

DR WPI; 1999-430039/36.

Ady55703 Human fib
Ady32457 Human fib
Aeb56257 Event seq
Aeb78061 Human DNA
Aeb7201 Human bla
Adq38575 Human SNP
Adl18477 Human pro
Adz26738 Human fib
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Adr66637 Human pro
Adr65953 Human pro
Acc06170 Human cDN
Acc00412 Human cel
Adz26740 Human fib
Adp64998 Human fib
Adg89565 Human fib
Adq29601 Human col
Adr67200 Human bla
Adv70129 Tumor-ass
Aeb17605 Human fib
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Adz26744 Human fib
Adz26748 Human fib
Adz26564 Human fib
Adz26742 Human fib
Adw81010 Fibronect
Adx69342 DNA encod
Adz26746 Human fib
Adq38578 Human SNP
Adq38582 Human SNP
Adq38583 Human SNP
Adq38577 Human SNP
Adq38586 Human SNP
Adg38579 Human FN
Aac89889 Human FN
Adq38584 Human SNP
Adq38574 Human SNP
Adq38587 Human SNP
Adq38576 Human SNP
Adq38580 Human SNP
Adj56196 Zebrafish

DR P-PSDB; AAY28901.
 XX Proteins with cell migration stimulatory activity used in treating wound
 PT and preventing scarring.

XX Example 1; Fig 1; 86pp; English.

XX The invention provides a human migration stimulatory factor (MSF)
 CC protein. Host cells containing a replicable vector comprising the MSF
 CC encoding nucleic acid can be used for the recombinant production of the
 CC protein. The polypeptide can be used for modulating cell migration,
 CC healing a wound and for preventing scarring. The present sequence
 CC represents the nucleotide sequence encoding a human MSF1-alpha protein

XX Sequence 2147 BP; 575 A; 512 C; 575 G; 485 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.19e-242 Length: 2147
 Score: 3687.00 Matches: 642
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-09-581-651D-2 (1-642) x AAX81299 (1-2147)

QY 1 MetLeuArgGlyProGlyProGlyLeuLeuLeuLeuAlaValGlnCysLeuGlyThrAla 20
 DB 57 ATGCTTAGGGGTCGGGGCCGGGGCTGCTGCTGCGCGCTGCAGTGCCTGGGGGACGCG 116
 QY 21 ValProSerThrGlyAlaSerLysSerLysArgGlnAlaGlnGlnMetValGlnProGln 40
 DB 117 GTCCCTCCACGGAGGCTCGAAGACGACGAGCGGCTCAGCAATGGTTGAGCCCCAG 176
 QY 41 SerProValAlaValSerGlnSerLysProGlyCysTyrAspAsnGlyLysHisTyrGln 60
 DB 177 TCCCGGTGCTGCTCAGTCAAGCAAGCCGGTGTGTATGACAAATGGAAACACTATCAG 236
 QY 61 IleAsnGlnInTrpGluArgThrTyrLeuGlyAsnAlaLeuValCysThrCysTyrGly 80
 DB 237 ATAAATCAACAGTGGGAGCGGACCTACCTAGGCAATGCGTGGTGTGTATGTTATGGA 296
 QY 81 GlySerArgGlyPheAsnCysGluSerLysProGluAlaGluGluThrCysPheAspLys 100
 DB 297 GGAAGCGAGGTTTAACTCGAGAGATTAACCTGAGAGCTGAAGAGACTTGTCTTGAAGA 356
 QY 101 TyrThrGlyAsnThrTyrArgValGlyAspThrTyrGluArgProLysAspSerMetIle 120
 DB 357 TACACTGGGAACACTTACCAGTGGGTGACACTTATGAGCGTCTTAAAGACTCCATGATC 416
 QY 121 TrpAspCysThrCysIleGlyAlaGlyArgGlyArgIleSerCysThrIleAlaAsnArg 140
 DB 417 TGGGACTGTACCTGCAATCGGGCTGGGCGAGGAGAAATAGCTGTATACCATCGCAACCGC 476
 QY 141 CysHisGluGlyGlnSerTyrLysIleGlyAspThrTrpArgArgProHisGluThr 160
 DB 477 TGCATGAAGGGGTGAGTCTTACACAGATTGGTGACACTCGGAGGAGACCAATGAGACT 536
 QY 161 GlyGlyTyrMetLeuGluCysValCysLeuGlyAsnGlyLysGlyGluTrpThrCysLys 180
 DB 537 GGTGGTTACATGTTAGATTGTGTGCTTGGTAAATGGAAAGGAAATGGACCTGCAAG 596
 QY 181 ProIleAlaGluCysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 200
 DB 597 CCATAGCTGAGAAGTGTGTGATCATGCTGCTGGGACTTCTCTATGTTGGTGGAGAAACG 656
 QY 201 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGluGlySer 220
 DB 657 TGGGAGAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAGGCAGC 716
 QY 221 GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 240
 DB 717 GGACGCATCACTTGCACTTCTAGAAATAGATGCAACGATCAGGACACAAAGGACATCCTAT 776

QY 241 ArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuLeuGlnCysIleCys 260
 DB 777 AGAATTTGGAGACACCTTGGAGCAAGAGATAATCGAGAAACCTGCTCCAGTCATCTGC 836
 QY 261 ThrGlyAsnGlyArgGlyGluTrpLysCysGluAatqHisThrSerValGlnThrThrSer 280
 DB 837 ACAGGACAGCGCGAGGAGAGTGGAAAGTGTGAGAGGCACACCTCTGTGACACACATCG 896
 QY 281 SerGlySerGlyProPheThrAspValArgAlaAlaValTyrGlnProGlnProHisPro 300
 DB 897 AGCGGATCTGGCCCTTCCCGATGTTCTGTCAGCTGTTTACCAACCGCAGCCTCACCCC 956
 QY 301 GlnProProProTyrGlyHisCysValThrAspSerGlyValValTyrSerValGlyMet 320
 DB 957 CAGCCTCTCCCTATGGCCACTGTGTCAACAGCAGTGGTGTGCTTACTCTGTGGGGATG 1016
 QY 321 GlnTrpLeuLysThrGlnGlyAsnLysGlnMetLeuCysThrCysLeuGlyAsnGlyVal 340
 DB 1017 CAGTGGCTGAGACACACAGGAAATTAAGCAATGCTTTGGACGCTGCTGGGCAACGAGTGC 1076
 QY 341 SerCysGlnGluThrAlaValThrGlnThrTyrGlyGlyAsnSerAsnGlyGluProCys 360
 DB 1077 AGCTGCCAAGACAGACTGTAAACCCAGACTTACGGTGGCACTCAAAATGGAGAGCCATGT 1136
 QY 361 ValLeuProPheThrTyrAsnAspArgThrAspSerThrThrSerAsnTyrGluGlnAsp 380
 DB 1137 GTCTTACCATTACCTTACCAACACAGGACGAGCAGACCAACTTCGAAATTTATGAGCAGGAC 1196
 QY 381 GlnLysTyrSerPheCysThrAspHisThrValLeuValGlnThrArgGlyGlyAsnSer 400
 DB 1197 CAGAAATACTCTTTCTGACACAGACCACACTGTTTGGTTTCAGACTCGAGAGGAAATTC 1256
 QY 401 AsnGlyAlaLeuCysHisPheProPheLeuTyrAsnAsnHisAsnTyrThrAspCysThr 420
 DB 1257 AATGCTGCTTGTGCCACTTCCCTTCTTATACAACACCACTATACACTGATTGCACT 1316
 QY 421 SerGluGlyArgArgAspAsnMetLysTrpCysGlyThrThrGlnAsnTyrAspAlaAsp 440
 DB 1317 TCTGAGGGCAGAGAGACAACTGAAGTGTGTGGGACCACACAGAACTATGATGCCGAC 1376
 QY 441 GlnLysPheGlyPheCysProMetAlaAlaHisGluGluIleCysThrThrAsnGluGly 460
 DB 1377 CAGAAATTTGGGTTCTGCCCATGGCTGCCACGAGGAAATCTGCACAACCAATGAAGGG 1436
 QY 461 ValMetTyrArgIleGlyAspGlnTrpAspLysGlnHisAspMetGlyHisMetMetArg 480
 DB 1437 GTCATGTACCGCATTTGGAGATCAGTGGGATAAGCAGCATGACATGGGTCACTGATGAGG 1496
 QY 481 CysThrCysValGlyAsnGlyArgGlyGluTrpThrCysIleAlaTyrSerGlnLeuArg 500
 DB 1497 TGCAGTGTGTGGGAATGGTCTGGGGAATGGACATGCTATTCCTTACTTCGCAGCTTCGA 1556
 QY 501 AspGlnCysIleValAspAspIleThrTyrAsnValAsnAspThrPheHisLysArgHis 520
 DB 1557 GATCAGTCATTTGTGATGACATCACTTACAATGTGAACGACACATTCACAAAGCGTCAT 1616
 QY 521 GluGluGlyHisMetLeuAsnCysThrCysPheGlyGlnGlyArgGlyArgTrpLysCys 540
 DB 1617 GAAAGGGGACATGCTGAACCTGTACATGCTTCGGTCAGGGTGGGGCAGGTGGAAGTGT 1676
 QY 541 AspProValAspGlnCysGlnAspSerGluThrGlyThrPheTyrGlnIleGlyAspSer 560
 DB 1677 GATCCCGTCGACCAATGCCAGATTCAGAGACTGGGAGCTTTTATCAAAATGGAGATTCA 1736
 QY 561 TrpGluLysTyrValHisGlyValArgTyrGlnCysTyrCysTyrGlyArgGlyIleGly 580
 DB 1737 TGGGAGAGATGTCATGGTGTGATACCACTGCTACTGCTATGGCGGTGGCATTTGGG 1796
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 DB 1797 GAGTGGCATTCGCAACCTTTACAGACCTTATCCAAGCTCAAGTGGTCTGTGTCGAAGTATTT 1856

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 12, 2006, 10:13:41 ; Search time 11858.3 Seconds
(without alignments)
4616.200 Million cell updates/sec

Title: US-09-581-651D-2

Perfect score: 3687

Sequence: 1 MLKCPGPGILLLLAVQCLGTA.....ISKYLKWRPVSPPPNRLGY 642

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=GenEmbl -OPMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -NATRIK=blom62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs04
-USER=US09581651 @CGN 1.1 5142 @runat.10052006.181206.153 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb.ba.*

2: gb.in.*

3: gb.env.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

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14: gb.htg.*

15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3687	100.0	2147	6	BD137021 Polypepti
2	3687	100.0	2147	6	AX003229 Sequence
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4	3680	99.8	1929	6	CQ871810	Sequence
5	3680	99.8	1929	6	CQ871828	Sequence
6	3680	99.8	2358	6	CQ875358	Sequence
7	3648.5	99.0	2192	8	HA535086	Homo sapi
8	3648.5	99.0	5984	8	AJ849445	Homo sapi
9	3638.5	98.7	4321	8	HS0806214	Homo sapi
10	3599.5	97.6	7242	6	CQ896577	Sequence
11	3599.5	97.6	7753	8	AB191261	Homo sapi
12	3599.5	97.6	8027	6	CQ833991	Sequence
13	3599.5	97.6	8027	6	CQ875357	Sequence
14	3599.5	97.6	8815	6	CS023820	Sequence
15	3599.5	97.6	8815	6	CS037064	Sequence
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17	3592.5	97.4	7745	8	AB209840	Homo sapi
18	3592.5	97.4	7951	8	HS0806901	Homo sapi
19	3592.5	97.4	7951	8	HS0806902	Homo sapi
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25	3585.5	97.2	7544	8	HS0803509	Homo sapi
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28	3578.5	97.1	7161	6	CS017033	Sequence
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33	3448.5	93.5	7680	6	AX335368	Sequence
34	3448.5	93.5	7680	6	HSFIB1	Human mRNA
35	3433.5	93.1	7705	6	A14133	Fibronectin
36	3433.5	93.1	7705	6	AR034630	Sequence
37	3433.5	93.1	7705	6	E01162	cDNA encodi
38	3433.5	93.1	7705	6	I70110	Sequence 16
39	3428.5	93.0	7705	6	AR364992	Sequence
40	3393.5	92.0	3059	9	BC051082	Mus muscu
41	3354.5	91.0	8329	9	AX402055	Sequence
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43	3289.5	89.2	6816	6	CQ715726	Sequence
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ALIGNMENTS

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DEFINITION	BD137021	Polypeptides, polynucleotides and uses thereof.			
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VERSION	BD137021.1	JP 2002508179-A/1.			
KEYWORDS	JP 2002508179-A/1.	Homo sapiens (human)			
SOURCE	JP 2002508179-A/1.	Homo sapiens			
ORGANISM	JP 2002508179-A/1.	Homo sapiens			
REFERENCE	JP 2002508179-A/1.	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
AUTHORS	JP 2002508179-A/1.	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
TITLE	JP 2002508179-A/1.	Hominidae; Homo.			
JOURNAL	JP 2002508179-A/1.	1 (bases 1 to 2147)			
COMMENT	JP 2002508179-A/1.	Schor, S.L. and Schor, A.M.			
	JP 2002508179-A/1.	Polypeptides, polynucleotides and uses thereof			
	JP 2002508179-A/1.	Patent: JP 2002508179-A 1 19-MAR-2002;			
	JP 2002508179-A/1.	UNIVERSITY OF DUNDEE			
	JP 2002508179-A/1.	OS Homo sapiens (human)			
	JP 2002508179-A/1.	PD 19-MAR-2002			
	JP 2002508179-A/1.	PR 15-DEC-1998 JP 2000539133			
	JP 2002508179-A/1.	PR 16-DEC-1997 GB 9726539.1			
	JP 2002508179-A/1.	PI SETH LAWRENCE SCHOR, ANA MARIA SCHOR			
	JP 2002508179-A/1.	PC C12N15/09,A61K38/00,A61P17/02,C07K14/78,C07K16/18,C12N5/10, PC			
	JP 2002508179-A/1.	C12P21/09,			
	JP 2002508179-A/1.	PC C12Q1/68,G01N33/574,C12N15/00,A61K37/02,C12N5/00 CC			
	JP 2002508179-A/1.	Polypeptides, polynucleotides and uses thereof. FH Key			

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		/mol_type="genomic DNA"		
		/db_xref="taxon:9606"		
ORIGIN				
Alignment Scores:				
Pred. No.:	3.5e-247	Length:	2147	
Score:	3687.00	Matches:	642	
Percent Similarity:	100.0%	Conservative:	0	
Best Local Similarity:	100.0%	Mismatches:	0	
Query Match:	100.0%	Indels:	0	
DB:	6	Gaps:	0	
US-09-581-651D-2 (1-642) x BD137021 (1-2147)				
Qy	1	MetLeuArgGlyProGlyProGlyLeuLeuLeuAlaValGlnCysLeuGlyThrAla	20	
Db	57	ATGCTTAGGGTCCGGGCCCCGGCTGCTGCTGCGCCCTCCAGTGCCTGGGACAGCG	116	
Qy	21	ValProSerThrGlyAlaSerLysSerLysArgGlnAlaGlnMetValGlnProGln	40	
Db	117	GTGCCCTCCACGGGAGCTCGAAGACCAAGAGGAGGAGGCTCAGCAATGGTTTCAGCCCCAG	176	
Qy	41	SerProValAlaValSerGlnSerLysProGlyCysTyrAspAsnGlyLysHisTyrGln	60	
Db	177	TCCCCGGTGGCTGTCAGTCAAGCAAGCCCGGTGTTTATGACAAATGGATGGAAACACTATCAG	236	
Qy	61	IleAsnGlnGlnTrpGluArgThrTyrLeuGlyAsnAlaLeuValCysThrCysTyrGly	80	
Db	237	ATAAATCAACAGTGGGAGCGGACCTACCTAGGCAATGCGTGGTGTGTTATGGA	296	
Qy	81	GlySerArgGlyPheAsnGlySerLysProGluAlaGluGlnThrCysPheAspLys	100	
Db	297	GGAAAGCCGAGTTTAACTGCGAGAGTAAACCTGAAAGCTGAAGAGACTTGCCTTTGACAAG	356	
Qy	101	TyrThrGlyAsnThrTyrArgValGlyAspThrTyrGluArgProLysAspSerMetIle	120	
Db	357	TACACTGGGAAACACTTACCGAGTGGGTGACACTTATGAGCGTCTTAAAGACTCCATGATC	416	
Qy	121	TrpAspCysThrCysIleGlyAlaGlyArgGlyArgIleSerCysThrIleAlaAsnArg	140	
Db	417	TGGGACTGTACCTGCAATCGGGGCTGGGCGAGGGAGATTAAGCTGTACATCGCAACCCGC	476	
Qy	141	CysHisGluGlyGlyGlnSerTyrLysIleGlyAspThrTrpArgArgProHisGluThr	160	
Db	477	TGCCATGAAGGGGTGAGTCTTACAGATTGGTGACACCTGGAGGAGACCATGAGACT	536	
Qy	161	GlyGlyTyrMetLeuGluCysValCysLeuGlyAsnGlyLysGlyGluTrpThrCysLys	180	
Db	537	GGTGGTTACATGTTAGAGTGTGTGCTTGGTAAATGGAAGAGAGATGGACCTGCAAG	596	
Qy	181	ProIleAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr	200	
Db	597	CCCATAGCTGAGAAGTGTGTTGATCATGCTGCTGGGACTTCCCTATGTGTGGGAGAAAGC	656	
Qy	201	TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGlySer	220	
Db	657	TGGGAGAAGCCCTACCAAGGCTGGATGATGTTAGATTGTTACTTGCCTGGGAGAGGCAGC	716	
Qy	221	GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr	240	
Db	717	GGACGCATCACTTGCATCTTCAAAATAGATGCAACGATCAGGACCAAGGACATCCTAT	776	
Qy	241	ArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuGlnCysIleCys	260	
Db	777	AGATTGGAGACACCTGGAGCAAGAGGATTAATCGAGGAACCTGCTCCAGTGCATCTGC	836	
Qy	261	ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer	280	

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 10, 2006, 19:42:45 ; Search time 38.4018 Seconds
(without alignments)
784.888 Million cell updates/sec

Title: US-09-581-651D-2

Perfect score: 3687

Sequence: 1 MLRGPGLLLAVQLCTA.....ISKYLWRPVSIPRNLGY 642

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 4694837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:*

- 1: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB.pepl.*
- 2: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pepl.*
- 3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pepl.*
- 4: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB.pepl.*
- 5: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB.pepl.*
- 6: /SIDSS/ptodata/2/pubpaa/US05_NEW_PUB.pepl.*
- 7: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pepl.*
- 8: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pepl.*
- 9: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pepl.*
- 10: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pepl.*
- 11: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pepl.*
- 12: /SIDSS/ptodata/2/pubpaa/US60_NEW_PUB.pepl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3664	99.4	642	9	US-10-995-561-631
2	3653.5	99.1	657	11	US-11-193-561-27
3	3653.5	99.1	657	11	US-11-193-771-21
4	3653.5	99.1	657	11	US-11-193-789-27
5	3653.5	99.1	657	11	US-11-193-806-27
6	3653.5	99.1	657	11	US-11-193-857-27
7	3646.5	98.9	657	9	US-10-995-561-622
8	3599.5	97.6	2176	11	US-11-193-561-25
9	3599.5	97.6	2176	11	US-11-193-771-25
10	3599.5	97.6	2176	11	US-11-193-789-25
11	3599.5	97.6	2176	11	US-11-193-806-25
12	3599.5	97.6	2176	11	US-11-193-857-25
13	3599.5	97.6	2217	11	US-11-193-561-38
14	3599.5	97.6	2217	11	US-11-193-771-38
15	3599.5	97.6	2217	11	US-11-193-789-38
16	3599.5	97.6	2217	11	US-11-193-806-38
17	3599.5	97.6	2217	11	US-11-193-857-38
18	3599.5	97.6	2296	11	US-11-193-561-23
19	3599.5	97.6	2296	11	US-11-193-771-23
20	3599.5	97.6	2296	11	US-11-193-789-23
21	3599.5	97.6	2296	11	US-11-193-806-23

22	3599.5	97.6	2296	11	US-11-193-857-23	Sequence 23, Appl
23	3599.5	97.6	2330	11	US-11-193-561-21	Sequence 21, Appl
24	3599.5	97.6	2330	11	US-11-193-771-21	Sequence 21, Appl
25	3599.5	97.6	2330	11	US-11-193-789-21	Sequence 21, Appl
26	3599.5	97.6	2330	11	US-11-193-806-21	Sequence 21, Appl
27	3599.5	97.6	2330	11	US-11-193-857-21	Sequence 21, Appl
28	3599.5	97.6	2355	11	US-11-193-561-19	Sequence 19, Appl
29	3599.5	97.6	2355	11	US-11-193-771-19	Sequence 19, Appl
30	3599.5	97.6	2355	11	US-11-193-789-19	Sequence 19, Appl
31	3599.5	97.6	2355	11	US-11-193-806-19	Sequence 19, Appl
32	3599.5	97.6	2355	11	US-11-193-857-19	Sequence 19, Appl
33	3599.5	97.6	2384	9	US-10-821-234-1545	Sequence 1545, Ap
34	3599.5	97.6	2421	11	US-11-193-561-17	Sequence 17, Appl
35	3599.5	97.6	2421	11	US-11-193-771-17	Sequence 17, Appl
36	3599.5	97.6	2421	11	US-11-193-789-17	Sequence 17, Appl
37	3599.5	97.6	2421	11	US-11-193-806-17	Sequence 17, Appl
38	3599.5	97.6	2421	11	US-11-193-857-17	Sequence 17, Appl
39	3599.5	97.6	2477	11	US-11-193-561-15	Sequence 15, Appl
40	3599.5	97.6	2477	11	US-11-193-771-15	Sequence 15, Appl
41	3599.5	97.6	2477	11	US-11-193-789-15	Sequence 15, Appl
42	3599.5	97.6	2477	11	US-11-193-806-15	Sequence 15, Appl
43	3599.5	97.6	2477	11	US-11-193-857-15	Sequence 15, Appl
44	3592.5	97.4	984	9	US-10-985-561-629	Sequence 629, App
45	3592.5	97.4	2296	9	US-10-995-561-633	Sequence 633, App

ALIGNMENTS

RESULT 1

US-10-995-561-631
; Sequence 631, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 631
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-631

Query Match	99.4%	Score 3664;	DB 9;	Length 642;
Best Local Similarity	99.5%	Pred. No. 9.7e-285;		
Matches 639;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	MLRGPGLLLAVQLCTA	VPSTGASKSRQAAQVQPSVAVSQSPGCGYDNGHYQ	60
Db	1	MLRGPGLLLAVLCLGTA	VPSTGASKSRQAAQVQPSVAVSQSPGCGYDNGHYQ	60
Qy	61	INQWERTYLGNAVCTCYG	SGSFNCESKPEAEETCFDKYTGNTYRVGDTYERPKDSMI	120
Db	61	INQWERTYLGNAVCTCYG	SGSFNCESKPEAEETCFDKYTGNTYRVGDTYERPKDSMI	120
Qy	121	WDCTCTGAGRGRTISCT	IANRCHGGGOSYKIGDTRRPHETGGYMLCEVCILGNKGWETCK	180
Db	121	WDCTCTGAGRGRTISCT	IANRCHGGGOSYKIGDTRRPHETGGYMLCEVCILGNKGWETCK	180
Qy	181	PIAEKCFDHAAGTSYV	VGTEWKEPYQGMWVDCITCLGEGSGRITCTSRNCNDQDRTSY	240
Db	181	PIAEKCFDHAAGTSYV	VGTEWKEPYQGMWVDCITCLGEGSGRITCTSRNCNDQDRTSY	240
Qy	241	RIGDTSWKONRGNLLQ	CICTGNRGWKCERHTSVQTTSSSGSPPTDVRAAVYQPOPH	300
Db	241	RIGDTSWKONRGNLLQ	CICTGNRGWKCERHTSVQTTSSSGSPPTDVRAAVYQPOPH	300

QY 301 QPPYGHCVTDSDGVVYVSGWQMLKTQGNKQMLCTCLNGVSCQETAVTQTYGNSNGEPC 360
DB 301 QPPYGHCVTDSDGVVYVSGWQMLKTQGNKQMLCTCLNGVSCQETAVTQTYGNSNGEPC 360
QY 361 VLPFTYNDRTSDTSNYEQDQKYSFCTDHTVLVQTRGNSNGALCHFPFLYNNHNTDCT 420
DB 361 VLPFTYNGRTCSITSNYEQDQKYSFCTDHTVLVQTRGNSNGALCHFPFLYNNHNTDCT 420
QY 421 SEGRDMMKCGTTONYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQDKQHDGMHMR 480
DB 421 SEGRDMMKCGTTONYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQDKQHDGMHMR 480
QY 481 CTCVNGRGWTCIAYSQLRDQCIYVDDITYNVNDTTHKRHEEGHMLNCTCFGGGRGWKC 540
DB 481 CTCVNGRGWTCIAYSQLRDQCIYVDDITYNVNDTTHKRHEEGHMLNCTCFGGGRGWKC 540
QY 541 DPVDCQDSETGTFTYQIGDSWEKYVHGVRVYQCYCGRGIGEMHCQPLQTYPSSSGPVEVF 600
DB 541 DPVDCQDSETGTFTYQIGDSWEKYVHGVRVYQCYCGRGIGEMHCQPLQTYPSSSGPVEVF 600
QY 601 ITETPSQPNSHPIQWNAPOQSHISKYLRLWRPVSIPPRLNGY 642
DB 601 ITETPSQPNSHPIQWNAPOQSHISKYLRLWRPVSIPPRLNGY 642

RESULT 2

US-11-193-561-27
; Sequence 27, Application US/11193561
; Publication No. US20060024757A1
; GENERAL INFORMATION:
; APPLICANT: Huesa, Robert
; APPLICANT: Shorter, Simon
; TITLE OF INVENTION: Detection of Oncofetal Fibronectin for Selection of Concepti
; FILE REFERENCE: 17101-080001/831
; CURRENT APPLICATION NUMBER: US/11/193,561
; PRIOR FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank NM 054034
; DATABASE ENTRY DATE: 2005-06-10
US-11-193-561-27

Query Match 99.1%; Score 3653.5; DB 11; Length 657;
Best Local Similarity 97.4%; Pred. No. 6.9e-284;
Matches 640; Conservative 0; Mismatches 2; Indels 15; Gaps 1;
QY 1 MLRGPGLLLAVQCLGTAVPSTGASKSRQAQQMVQPSVAVSQSKPGCYDNGKHQY 60
DB 1 MLRGPGLLLAVQCLGTAVPSTGASKSRQAQQMVQPSVAVSQSKPGCYDNGKHQY 60
QY 61 INQWERTYLGALVCTCYGSGRGFNCESKPEAEETCFDKYTGNTYRVGDTYERPKDSMI 120
DB 61 INQWERTYLGALVCTCYGSGRGFNCESKPEAEETCFDKYTGNTYRVGDTYERPKDSMI 120
QY 121 WDCTCIGAGRGRTSCTIANRCHGGGQSYKIGDTPRRPHETGGVYMLBVCVLGNGKGWTC 180
DB 121 WDCTCIGAGRGRTSCTIANRCHGGGQSYKIGDTPRRPHETGGVYMLBVCVLGNGKGWTC 180

QY 181 PLAEKCFDHAAGTSYVVGETWEKPYQGMWMMVDTCLGEGSGRITCTSRNRCNDQDTRTSY 240
DB 181 PLAEKCFDHAAGTSYVVGETWEKPYQGMWMMVDTCLGEGSGRITCTSRNRCNDQDTRTSY 240
QY 241 RIGDTWSKKDNRGNLLQCICTGNGRGEMKCRHSTSVQTTSSGSGPFTDVRAAVYQPPHP 300
DB 241 RIGDTWSKKDNRGNLLQCICTGNGRGEMKCRHSTSVQTTSSGSGPFTDVRAAVYQPPHP 300
QY 301 QPPYGHCVTDSDGVVYVSGWQMLKTQGNKQMLCTCLNGVSCQETAVTQTYGNSNGEPC 360
DB 301 QPPYGHCVTDSDGVVYVSGWQMLKTQGNKQMLCTCLNGVSCQETAVTQTYGNSNGEPC 360
QY 361 VLPFTYNDRTSDTSNYEQDQKYSFCTDHTVLVQTRGNSNGALC 405
DB 361 VLPFTYNGRTFSCTTEGQDHLNCTTSNYEQDQKYSFCTDHTVLVQTRGNSNGALC 420
QY 406 HFPFLYNNHNTDCTSEGRDMMKCGTTONYDADQKFGFCPMAAHEEICTTNEGVMYRI 465
DB 421 HFPFLYNNHNTDCTSEGRDMMKCGTTONYDADQKFGFCPMAAHEEICTTNEGVMYRI 480
QY 466 GDQWDKQHDGMHMRCTCVNGRGWTCIAYSQLRDQCIYVDDITYNVNDTTHKRHEEGHM 525
DB 481 GDQWDKQHDGMHMRCTCVNGRGWTCIAYSQLRDQCIYVDDITYNVNDTTHKRHEEGHM 540
QY 526 LNCTCFGGGRGWKCDPVDCQDSETGTFTYQIGDSWEKYVHGVRVYQCYCGRGIGEMHCQ 585
DB 541 LNCTCFGGGRGWKCDPVDCQDSETGTFTYQIGDSWEKYVHGVRVYQCYCGRGIGEMHCQ 600
QY 586 PLQTYPSSSGPVEVFITETPSQPNSHPIQWNAPOQSHISKYLRLWRPVSIPPRLNGY 642
DB 601 PLQTYPSSSGPVEVFITETPSQPNSHPIQWNAPOQSHISKYLRLWRPVSIPPRLNGY 657

RESULT 3

US-11-193-771-27
; Sequence 27, Application US/11193771
; Publication No. US20060024722A1
; GENERAL INFORMATION:
; APPLICANT: Fisher-Colbrie, Mark
; APPLICANT: Hickok, Durin
; APPLICANT: LaPointe, Jerome P.
; TITLE OF INVENTION: Samples for Detection of Oncofetal Fibronectin and uses thereof
; FILE REFERENCE: 17101-027001/828
; CURRENT APPLICATION NUMBER: US/11/193,771
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank NM 054034
; DATABASE ENTRY DATE: 2005-06-10
US-11-193-771-27

Query Match 99.1%; Score 3653.5; DB 11; Length 657;
Best Local Similarity 97.4%; Pred. No. 6.9e-284;
Matches 640; Conservative 0; Mismatches 2; Indels 15; Gaps 1;

QY 1 MLRGPGLLLAVQCLGTAVPSTGASKSRQAQQMVQPSVAVSQSKPGCYDNGKHQY 60
DB 1 MLRGPGLLLAVQCLGTAVPSTGASKSRQAQQMVQPSVAVSQSKPGCYDNGKHQY 60

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 10, 2006, 19:41:10 ; Search time 243.212 Seconds
(without alignments)
1102.934 Million cell updates/sec

Title: US-09-581-651D-2
Perfect score: 3687
Sequence: 1 MLRGPGLLLAVQCLGTA.....ISKYLRRPVSIPPRNLGY 642

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3664	99.4	642	4	US-10-741-601-354
2	3664	99.4	642	5	US-10-741-600-1066
3	3646.5	98.9	657	4	US-10-741-601-359
4	3646.5	98.9	657	5	US-10-741-600-1072
5	3599.5	97.6	2220	4	US-10-236-392-4
6	3599.5	97.6	2355	4	US-10-144-194A-104
7	3599.5	97.6	2355	4	US-10-447-161-3
8	3599.5	97.6	2355	4	US-10-734-564-94
9	3599.5	97.6	2355	5	US-10-491-566-104
10	3599.5	97.6	2355	5	US-10-852-335A-147
11	3599.5	97.6	2355	5	US-10-287-436A-436
12	3599.5	97.6	2355	5	US-10-287-436A-1137
13	3599.5	97.6	2355	6	US-11-040-130-28
14	3599.5	97.6	2386	5	US-10-618-281-32
15	3595.5	97.5	2386	3	US-09-961-403-1
16	3595.5	97.5	2386	4	US-10-788-792-206
17	3595.5	97.5	2386	5	US-10-868-577A-59
18	3595.5	97.5	2386	5	US-10-485-758-4
19	3595.5	97.5	2386	5	US-10-485-758-9
20	3592.5	97.4	984	4	US-10-741-601-356
21	3592.5	97.4	984	5	US-10-741-600-1069
22	3592.5	97.4	2296	4	US-10-741-601-363
23	3592.5	97.4	2296	5	US-10-741-600-1075
24	3592.5	97.4	2355	4	US-10-741-601-357
25	3592.5	97.4	2355	4	US-10-741-601-366
26	3592.5	97.4	2355	5	US-10-741-600-1067
27	3592.5	97.4	2355	5	US-10-741-600-1078

28	3592.5	97.4	2386	4	US-10-741-601-360	Sequence 360, App
29	3592.5	97.4	2386	5	US-10-741-600-1071	Sequence 1071, App
30	3505.5	95.1	2474	5	US-10-450-763-52638	Sequence 52638, A
31	3448.5	93.5	2328	4	US-10-171-311-64	Sequence 64, Appl
32	3448.5	93.5	2328	4	US-10-236-031B-70	Sequence 70, Appl
33	3448.5	93.5	2328	4	US-10-374-979-98	Sequence 98, Appl
34	3448.5	93.5	2328	4	US-10-182-936A-98	Sequence 677, App
35	3448.5	93.5	2328	5	US-10-477-238A-677	Sequence 98, Appl
36	3448.5	93.5	2328	5	US-10-680-287A-677	Sequence 677, App
37	3448.5	93.5	2328	5	US-10-477-173-677	Sequence 677, App
38	3439.5	93.3	2355	4	US-10-360-101-235	Sequence 235, App
39	3424.5	92.9	2320	4	US-10-279-733-8	Sequence 8, Appli
40	3410.5	92.5	2320	4	US-10-236-392-2	Sequence 2, Appli
41	3296.5	89.4	1173	5	US-10-450-763-52634	Sequence 52634, A
42	2141	58.1	463	4	US-10-144-194A-52	Sequence 52, Appl
43	2141	58.1	463	5	US-10-491-566-52	Sequence 52, Appl
44	1859.5	50.4	343	3	US-09-934-706-1	Sequence 1, Appli
45	1859.5	50.4	400	3	US-09-934-706-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-741-601-354
; Sequence 354, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 354
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-354

Query Match 99.4%; Score 3664; DB 4; Length 642;
Best Local Similarity 99.5%; Pred. No. 1.2e-289;
Matches 639; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MLRGPGLLLAVQCLGTA	VPSTGASKSRQQAQMVQPSVAVSQKPCGCDYNGKHQY	60
Db	1	MLRGPGLLLAVQCLGTA	VPSTGASKSRQQAQMVQPSVAVSQKPCGCDYNGKHQY	60
Qy	61	INQWERTYLGNA	LVCTCYGSGRGFNCESKPEAEETCFDKYTGTVRVGDTYERPKDSMI	120
Db	61	INQWERTYLGNA	LVCTCYGSGRGFNCESKPEAEETCFDKYTGTVRVGDTYERPKDSMI	120
Qy	121	WDCTCIGAGRGRI	SCTIANRCHGGQSYKIGDTRWRPHETGGYMLCEVCLGNGKGEWTK	180
Db	121	WDCTCIGAGRGRI	SCTIANRCHGGQSYKIGDTRWRPHETGGYMLCEVCLGNGKGEWTK	180
Qy	181	PIAEKCFDHAAGT	SYVVGTEWXPYQGMWMDCTCLGEGSGRITCTSRNRCNDQDTRTSY	240
Db	181	PIAEKCFDHAAGT	SYVVGTEWXPYQGMWMDCTCLGEGSGRITCTSRNRCNDQDTRTSY	240
Qy	241	RIGDTSWKDNRN	LLQCLCTGNGRGKCEHRTSVQTTSSGSGPFTDVRAAVYQPPHP	300
Db	241	RIGDTSWKDNRN	LLQCLCTGNGRGKCEHRTSVQTTSSGSGPFTDVRAAVYQPPHP	300
Qy	301	QPPYPGHCVTD	SGVYVSVGNQWLKTQGNKQMLCTCLGNGVSCQETAVTQTYGNSNGEPC	360
Db	301	QPPYPGHCVTD	SGVYVSVGNQWLKTQGNKQMLCTCLGNGVSCQETAVTQTYGNSNGEPC	360
Qy	361	VLPTVNDRTD	STTSNYEQDKYSFCTDHTVLVQTRGNSNGALCHFPFLYNNHNTDCT	420
Db	361	VLPTVNDRTD	STTSNYEQDKYSFCTDHTVLVQTRGNSNGALCHFPFLYNNHNTDCT	420

QY 421 SEGRDNNKWCCTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQDKQHDGMHMR 480
 DB 421 SEGRDNNKWCCTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQDKQHDGMHMR 480
 QY 481 CTCVNGRGWETCIAYSQLRDQCIYDQKFGFCPMAAHEEICTTNEGVMYRIGDQDKQHDGMHMR 540
 DB 481 CTCVNGRGWETCIAYSQLRDQCIYDQKFGFCPMAAHEEICTTNEGVMYRIGDQDKQHDGMHMR 540
 QY 541 DPVDCQDSEGTGTFFQIGDSWEKYVHGVRVQCYCYGRGIGEWHCQPLQTYPSSSGPVEVF 600
 DB 541 DPVDCQDSEGTGTFFQIGDSWEKYVHGVRVQCYCYGRGIGEWHCQPLQTYPSSSGPVEVF 600
 QY 601 ITETPSQPNSHPIQWNAPOQSHISKYILRWRPVSIPPRNLGY 642
 DB 601 ITETPSQPNSHPIQWNAPOQSHISKYILRWRPVSIPPRNLGY 642
 RESULT 2
 US-10-741-600-1066
 ; Sequence 1066, Application US/10741600
 ; Publication No. US20050026169A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001499
 ; CURRENT APPLICATION NUMBER: US/10/741,600
 ; CURRENT FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 73997
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1066
 ; LENGTH: 642
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-741-600-1066

Query Match 99.4%; Score 3664; DB 5; Length 642;
 Best Local Similarity 99.5%; Pred. No. 1.2e-289;
 Matches 639; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MLRGPGLLLAVCLGTAVPSTGASKSKRQAQMVQPQSPVAVSQSKPGCYDNGKHQ 60
 DB 1 MLRGPGLLLAVCLGTAVPSTGASKSKRQAQMVQPQSPVAVSQSKPGCYDNGKHQ 60
 QY 61 INQWERTYLGNAVCTCYGSGRGNFNCESKPEABETCFDKYTGNTYRVGDTYVERPKDSMI 120
 DB 61 INQWERTYLGNAVCTCYGSGRGNFNCESKPEABETCFDKYTGNTYRVGDTYVERPKDSMI 120
 QY 121 WDCTCIGAGRGRIISCTIANRCHEGGQSYKIGDWRPHETGGYMLCEVCLGNGKGWTC 180
 DB 121 WDCTCIGAGRGRIISCTIANRCHEGGQSYKIGDWRPHETGGYMLCEVCLGNGKGWTC 180
 QY 181 PIAEKCFDHAAGTSYVVGTEWKPQGMWVDCCTCLGEGSGRITCTSRNRCNDQDTRTSY 240
 DB 181 PIAEKCFDHAAGTSYVVGTEWKPQGMWVDCCTCLGEGSGRITCTSRNRCNDQDTRTSY 240
 QY 241 RIGDTSWKDNRNLLQCICTGNGRGWKCERHTSVQTTSSGSGPFTDVRAAVYQPPHP 300
 DB 241 RIGDTSWKDNRNLLQCICTGNGRGWKCERHTSVQTTSSGSGPFTDVRAAVYQPPHP 300
 QY 301 QPPPYGHCVTDSGVVYVSGMQLKTOGNKQMLCTCLGNGVSCQETAVTQTYGNSNGEPC 360
 DB 301 QPPPYGHCVTDSGVVYVSGMQLKTOGNKQMLCTCLGNGVSCQETAVTQTYGNSNGEPC 360
 QY 361 VLPFTYNDRTSTTSNYEQDQKYSFCTDHTVLVQTRGNSNGALC 405
 DB 361 VLPFTYNDRTSTTSNYEQDQKYSFCTDHTVLVQTRGNSNGALC 405
 QY 406 HPFFLYNNHNYTDCSTSEGRDNNKWCCTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRI 465
 DB 406 HPFFLYNNHNYTDCSTSEGRDNNKWCCTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRI 465
 QY 421 SEGRDNNKWCCTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQDKQHDGMHMR 480
 DB 421 SEGRDNNKWCCTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQDKQHDGMHMR 480

QY 481 CTCVNGRGWETCIAYSQLRDQCIYDQKFGFCPMAAHEEICTTNEGVMYRIGDQDKQHDGMHMR 540
 DB 481 CTCVNGRGWETCIAYSQLRDQCIYDQKFGFCPMAAHEEICTTNEGVMYRIGDQDKQHDGMHMR 540
 QY 541 DPVDCQDSEGTGTFFQIGDSWEKYVHGVRVQCYCYGRGIGEWHCQPLQTYPSSSGPVEVF 600
 DB 541 DPVDCQDSEGTGTFFQIGDSWEKYVHGVRVQCYCYGRGIGEWHCQPLQTYPSSSGPVEVF 600
 QY 601 ITETPSQPNSHPIQWNAPOQSHISKYILRWRPVSIPPRNLGY 642
 DB 601 ITETPSQPNSHPIQWNAPOQSHISKYILRWRPVSIPPRNLGY 642
 RESULT 3
 US-10-741-601-359
 ; Sequence 359, Application US/10741601
 ; Publication No. US20040166519A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001500
 ; CURRENT APPLICATION NUMBER: US/10/741,601
 ; CURRENT FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 26415
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 359
 ; LENGTH: 657
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-741-601-359

Query Match 98.9%; Score 3646.5; DB 4; Length 657;
 Best Local Similarity 97.3%; Pred. No. 3.4e-288;
 Matches 639; Conservative 0; Mismatches 3; Indels 15; Gaps 1;
 QY 1 MLRGPGLLLAVCLGTAVPSTGASKSKRQAQMVQPQSPVAVSQSKPGCYDNGKHQ 60
 DB 1 MLRGPGLLLAVCLGTAVPSTGASKSKRQAQMVQPQSPVAVSQSKPGCYDNGKHQ 60
 QY 61 INQWERTYLGNAVCTCYGSGRGNFNCESKPEABETCFDKYTGNTYRVGDTYVERPKDSMI 120
 DB 61 INQWERTYLGNAVCTCYGSGRGNFNCESKPEABETCFDKYTGNTYRVGDTYVERPKDSMI 120
 QY 121 WDCTCIGAGRGRIISCTIANRCHEGGQSYKIGDWRPHETGGYMLCEVCLGNGKGWTC 180
 DB 121 WDCTCIGAGRGRIISCTIANRCHEGGQSYKIGDWRPHETGGYMLCEVCLGNGKGWTC 180
 QY 181 PIAEKCFDHAAGTSYVVGTEWKPQGMWVDCCTCLGEGSGRITCTSRNRCNDQDTRTSY 240
 DB 181 PIAEKCFDHAAGTSYVVGTEWKPQGMWVDCCTCLGEGSGRITCTSRNRCNDQDTRTSY 240
 QY 241 RIGDTSWKDNRNLLQCICTGNGRGWKCERHTSVQTTSSGSGPFTDVRAAVYQPPHP 300
 DB 241 RIGDTSWKDNRNLLQCICTGNGRGWKCERHTSVQTTSSGSGPFTDVRAAVYQPPHP 300
 QY 301 QPPPYGHCVTDSGVVYVSGMQLKTOGNKQMLCTCLGNGVSCQETAVTQTYGNSNGEPC 360
 DB 301 QPPPYGHCVTDSGVVYVSGMQLKTOGNKQMLCTCLGNGVSCQETAVTQTYGNSNGEPC 360
 QY 361 VLPFTYNDRTSTTSNYEQDQKYSFCTDHTVLVQTRGNSNGALC 405
 DB 361 VLPFTYNDRTSTTSNYEQDQKYSFCTDHTVLVQTRGNSNGALC 405
 QY 406 HPFFLYNNHNYTDCSTSEGRDNNKWCCTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRI 465
 DB 406 HPFFLYNNHNYTDCSTSEGRDNNKWCCTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRI 465
 QY 421 SEGRDNNKWCCTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQDKQHDGMHMR 480
 DB 421 SEGRDNNKWCCTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQDKQHDGMHMR 480
 QY 466 GDQWDKQHDGMHMRCTCVNGRGWETCIAYSQLRDQCIYDQKFGFCPMAAHEEICTTNEGVMYRI 525
 DB 466 GDQWDKQHDGMHMRCTCVNGRGWETCIAYSQLRDQCIYDQKFGFCPMAAHEEICTTNEGVMYRI 525
 QY 481 GDQWDKQHDGMHMRCTCVNGRGWETCIAYSQLRDQCIYDQKFGFCPMAAHEEICTTNEGVMYRI 540
 DB 481 GDQWDKQHDGMHMRCTCVNGRGWETCIAYSQLRDQCIYDQKFGFCPMAAHEEICTTNEGVMYRI 540
 QY 526 LNCTCFGQGRGWKCDPVDQDSEGTGTFFQIGDSWEKYVHGVRVQCYCYGRGIGEWHCQ 585

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OM protein - protein search, using sw model

Run on: May 10, 2006, 19:13:45 ; Search time 303.276 Seconds
(without alignments)
1493.521 Million cell updates/sec

Title: US-09-581-651D-2
Perfect score: 3687
Sequence: 1 MLRGPGLLLAVQCLGTA.....ISKYLWRPVSIPRNLGY 642

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3648.5	99.0	657	2	Q564H7 HUMAN
2	3638.5	98.7	749	2	Q72391 HUMAN
3	3599.5	97.6	2217	2	Q585T2 HOMO SAPIEN
4	3599.5	97.6	2265	2	Q60FE4 HOMO SAPIEN
5	3595.5	97.5	2386	1	F1NC HUMAN
6	3592.5	97.4	1103	2	Q6MZF4 HUMAN
7	3592.5	97.4	2296	2	Q6N0A6 HUMAN
8	3592.5	97.4	2351	2	Q59EH1 HUMAN
9	3592.5	97.4	2477	2	Q6MZU5 HUMAN
10	3591.5	97.4	2357	2	Q68DT4 HUMAN
11	3588.5	97.3	2267	2	Q68DP9 HUMAN
12	3588.5	97.3	2444	2	Q6N025 HUMAN
13	3567.5	96.8	2240	2	Q68DP8 HUMAN
14	3393.5	92.0	2477	1	F1NC MOUSE
15	3354.5	91.0	2477	1	F1NC RAT
16	3328.5	90.3	2265	1	F1NC BOVIN
17	2897	78.6	2475	2	Q501R6 XENTR
18	2888	78.3	2481	2	Q6GQ45 XENLA
19	2878	78.1	2481	1	F1NC XENLA
20	2513.5	68.2	922	2	Q93405 BRARE
21	2513.5	68.2	2478	2	Q93406 BRACHYDANIO
22	2383	64.6	1395	2	Q4SHU0 TETNG
23	2328	63.1	2408	2	Q6JAN2 BRARE
24	2314	62.8	2500	2	Q58XP5 BRARE
25	2201.5	52.7	2383	2	Q48NC4 TETNG
26	1942.5	52.7	360	2	Q5RLI3 PIG
27	1909.5	51.8	2193	2	Q6MZM7 HOMO SAPIEN
28	1817	49.3	383	2	Q4KL80 MOUSE
29	1496	40.6	296	2	Q8C6J7 MOUSE
30	1303	35.3	231	2	Q5MD86 MACMU
31	961	26.1	190	1	F1NC NOTVI

32	750	20.3	141	2	Q90XQ2 AMBME	Q90xq2 ambystoma m
33	541	14.7	215	2	Q6DD34 XENLA	Q6dd34 xenopus lae
34	331	9.0	410	2	Q4RVU5 TETNG	Q4rvu5 tetraodon n
35	319	8.7	677	2	Q4JF83 FUGR	Q4jf83 fuigu rubrip
36	317.5	8.6	679	2	Q98856 CYNPY	Q98856 cynops pyrr
37	313.5	8.5	673	2	Q90YB3 PAROL	Q90yb3 paralichthy
38	310.5	8.4	690	2	Q9PVM5 ORYLA	Q9pvm5 oryzias lat
39	307.5	8.3	679	2	Q5D7I3 NOTVI	Q5d7i3 notophthalm
40	307	8.3	670	2	Q6DFI6 XENTR	Q6dfi6 xenopus tro
41	307	8.3	680	2	Q7T3I7 BRARE	Q7t3i7 brachydanio
42	306	8.3	675	2	Q8QFO6 ONCMY	Q8qf6 oncorhynch
43	302.5	8.2	810	2	Q8R3F3 MOUSE	Q8r3f3 mus musculu
44	302	8.2	671	2	Q9W7L6 XENLA	Q9w7l6 xenopus lae
45	302	8.2	671	2	Q6PF33 XENLA	Q6pf33 xenopus lae

ALIGNMENTS

RESULT 1

ID	Q564H7 HUMAN PRELIMINARY;	PRT;	657 AA.
AC	Q564H7;		
DT	10-MAY-2005 (TrEMBLrel. 30, Created)		
DT	10-MAY-2005 (TrEMBLrel. 30, Last sequence update)		
DT	10-MAY-2005 (TrEMBLrel. 30, Last annotation update)		
DE	Migration stimulating factor.		
OS	Name=FN1;		
GN	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Kay R.A.M., Ellis I.R., Jones S.J., Perrier S., Florence M.M.,		
RA	Schor A.M., Schor S.L.;		
RT	"mRNA 3'-UTR truncation: a novel mechanism regulating gene		
RT	expression."		
RL	Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ849445; CAH60958.1; -; -;		
DR	SMR; Q564H7; 48-140, 183-275, 305-464.		
DR	Ensembl; ENSG00000115414; Homo sapiens.		
DR	GO; GO:0005576; C:extracellular region; IEA.		
DR	InterPro; IPR006209; EGF-like.		
DR	InterPro; IPR000083; Fibrinctnl.		
DR	InterPro; IPR000562; FN type2 col bd.		
DR	InterPro; IPR001724; Glyco_hydro_58.		
DR	Pfam; PF00039; fn1; 9.		
DR	Pfam; PF00040; fn2; 2.		
DR	PRINTS; PR00012; FNTYPEI.		
DR	PRINTS; PR00013; FNTYPEII.		
DR	PRINTS; PR00849; GLHYDLASE58.		
DR	SMART; SM00058; FN1; 9.		
DR	SMART; SM00059; FN2; 2.		
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.		
DR	PROSITE; PS01253; FN1_1; 9.		
DR	PROSITE; PS01091; FN1_2; 9.		
DR	PROSITE; PS00023; FN2_1; 2.		
DR	PROSITE; PS01092; FN2_2; 2.		
KW	Repeat.		
SQ	SEQUENCE 657 AA; 73752 MW; 8CA04E64486ABCD0 CRC64;		
Query Match 99.0%; Score 3648.5; DB 2; Length 657;			
Best Local Similarity 97.3%; Pred. No. 1.2e-263;			
Matches 639; Conservative 0; Mismatches 3; Indels 15; Gaps 1;			
Qy	1	MLRGPGLLLAVQCLGTAVPTGASKSKRQAQWVQPSVAVSQKPGCYDNGKHQY	60
Db	1	MLRGPGLLLAVQCLGTAVPTGASKSKRQAQWVQPSVAVSQKPGCYDNGKHQY	60
Qy	61	INQWERTYLGNALVCTCYGSGRGFNCSKPEAEETCFDKYTGTVRVGTYERPKDSMI	120

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OM protein - protein search, using sw model

Run on: May 10, 2006, 19:20:36 ; Search time 49.2331 Seconds
(without alignments)
1254.667 Million cell updates/sec

Title: US-09-581-651D-2
Perfect score: 3687
Sequence: 1 MLRPGGCLLLAVQCLGTA.....ISKYLWRPVPSPRNLGY 642

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3579.5	97.1	2386	1 FNHU	fibronectin precur
2	3354.5	91.0	2477	2 S14428	fibronectin precur
3	3328.5	90.3	2265	1 FNBO	fibronectin - bovi
4	2888	78.3	2481	2 A43908	fibronectin - Afri
5	961	26.1	190	2 I51279	fibronectin - east
6	302.5	8.2	708	2 JC4364	gelatinase B (EC 3
7	301	8.2	662	2 S70365	gelatinase A (EC 3
8	300	8.1	662	2 A42496	gelatinase A (EC 3
9	300	8.1	662	2 S34780	gelatinase A (EC 3
10	300	8.1	707	1 A53796	gelatinase B (EC 3
11	298	8.1	663	1 S46492	gelatinase A (EC 3
12	297	8.1	660	1 A28153	gelatinase A (EC 3
13	294.5	8.0	708	2 S62907	gelatinase B (EC 3
14	294.5	8.0	712	1 I46031	gelatinase B (EC 3
15	294.5	8.0	730	1 I52580	gelatinase B (EC 3
16	294.5	8.0	730	2 JC1456	gelatinase B (EC 3
17	285.5	7.7	707	1 A34458	gelatinase B (EC 3
18	228.5	6.2	1020	2 A29355	fibronectin - chic
19	208	5.6	1455	1 A48925	mannose receptor p
20	199.5	5.4	1456	1 A36563	mannose receptor p
21	199	5.4	5376	2 T42215	zonadhesin - mouse
22	190.5	5.2	1479	2 T42710	mannose receptor,
23	188	5.1	1458	1 A49707	phospholipase A2 r
24	185.5	5.0	1326	2 B56395	secretory phosphol
25	185.5	5.0	1465	2 A56395	secretory phosphol
26	185	5.0	1584	2 T22674	hypothetical prote
27	181.5	4.9	473	2 A56375	adhesive plaque pr
28	179.5	4.9	722	2 I48324	DELTA-like 1 - mou
29	179.5	4.9	1463	2 A53210	phospholipase A2 r

ALIGNMENTS

RESULT 1

FNHU

fibronectin precursor [validated] - human

N;Alternate names: fibronectin splice form ED-A

C;Species: Homo sapiens (man)

C;Date: 27-Nov-1985 #sequence revision 31-Mar-1993 #text change 31-Dec-2004

C;Accession: A26460; A26284; S03917; A24854; A24476; A91008; A93529; A21011; A90495; A22

R;Dean, D.C.; Bowlus, C.L.; Bourgeois, S.

Proc. Natl. Acad. Sci. U.S.A. 84, 1876-1880, 1987

A;Title: Cloning and analysis of the promoter region of the human fibronectin gene.

A;Reference number: A26460; MUID:87175578; PMID:3031656

A;Accession: A26460

A;Molecule type: DNA

A;Residues: 1-49 <DEA>

A;Cross-references: UNIPROT:P02751; UNIPROT:Q14327; UNIPARC:UPI000016A926; GB:M15801; NI

R;Oldberg, A.; Ruoslahti, E.

J. Biol. Chem. 261, 2113-2116, 1986

A;Title: Evolution of the fibronectin gene.

A;Reference number: A26284; MUID:86111901; PMID:3003095

A;Accession: A26284

A;Molecule type: DNA

A;Residues: 1447-1540 <OLD>

A;Cross-references: UNIPARC:UPI0000112E37; GB:M12549; NID:G182698

A;Note: the authors translated the codon TTC for residue 1494 as Glu

R;Paolella, G.; Henschcliff, C.; Sebastio, G.; Baralle, F.E.

Nucleic Acids Res. 16, 3545-3557, 1988

A;Title: Sequence analysis and in vivo expression show that alternative splicing of ED-B

A;Reference number: S00848; MUID:88233940; PMID:3375063

A;Accession: S03917

A;Molecule type: DNA

A;Residues: 1594-1767, 'V', 1769-1783 <PAO>

A;Cross-references: UNIPARC:UPI000017432B; EMBL:X07718; NID:G31402

A;Note: the authors translated the codon AAC for residue 1631 as Asp

R;Vibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.

FEBS Lett. 207, 287-291, 1986

A;Title: Donor and acceptor splice signals within an exon of the human fibronectin gene:

A;Reference number: A24854; MUID:87030929; PMID:3770201

A;Accession: A24854

A;Molecule type: DNA

A;Residues: 1992-2147 <VIB>

A;Cross-references: UNIPARC:UPI000017432C; GB:X04530; NID:G31436

R;Gutman, A.; Yamada, K.M.; Kornblihtt, A.

FEBS Lett. 207, 145-148, 1986

A;Title: Human fibronectin is synthesized as a pre-propolypeptide.

A;Reference number: A24476; MUID:87030890; PMID:3770189

A;Accession: A24476

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-14, 'Q', 16-38 <GUT>

A;Cross-references: UNIPARC:UPI000017432D

R;Kornblihtt, A.R.; Umezawa, K.; Vibe-Pedersen, K.; Baralle, F.E.

EMBO J. 4, 1755-1759, 1985

A;Title: Primary structure of human fibronectin: differential splicing may generate at l
A;Reference number: A91008; MUID:85284965; PMID:2992939
A;Accession: A91008
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 32-1344,1346-2080,2112-2386 <KOR>
A;Cross-references: UNIPARC:UPI0000174332; UNIPARC:UPI000017432F; GB:X02761
R;Kornblitt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Nucleic Acids Res. 12, 5853-5868, 1984
A;Title: Human fibronectin: cell specific alternative mRNA splicing generates polypeptid
A;Reference number: A93529; MUID:84272258; PMID:6462919
A;Accession: A93529
A;Molecule type: mRNA
A;Residues: 973-2080,2112-2386 <K02>
A;Cross-references: UNIPARC:UPI000017432F; UNIPARC:UPI0000174330; GB:X00739
R;Oldberg, A.; Linney, E.; Ruoslahti, E.
J. Biol. Chem. 258, 10193-10196, 1983
A;Title: Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell a
A;Reference number: A21011; MUID:83290929; PMID:6688418
A;Accession: A21011
A;Molecule type: mRNA
A;Residues: 1434-1537 <OL2>
A;Cross-references: UNIPARC:UPI0000174331; GB:K00055; NID:g182680; PIDN:AAAS2459.1; PID:
R;Bernard, M.P.; Kolbe, M.; Weil, D.; Chu, M.L.
Biochemistry 24, 2698-2704, 1985
A;Title: Human cellular fibronectin: comparison of the carboxyl-terminal portion with ra
A;Reference number: A90495; MUID:85280409; PMID:2992573
A;Accession: A90495
A;Molecule type: mRNA
A;Residues: 1594-2386 <BER>
A;Cross-references: UNIPARC:UPI000016A928; GB:M10905; NID:g182696; PIDN:AAAS2462.1; PID:
R;Umezawa, K.; Kornblitt, A.R.; Baralle, F.E.
FEBS Lett. 186, 31-34, 1985
A;Title: Isolation and characterization of cDNA clones for human liver fibronectin.
A;Reference number: A22245; MUID:85231203; PMID:2989004
A;Accession: A22245
A;Molecule type: mRNA
A;Residues: 1948-2067 <UME>
A;Cross-references: UNIPARC:UPI000000046A; GB:M27589; NID:g182705; PIDN:AAAS2465.1; PID:
A;Accession: B22245
A;Molecule type: mRNA
A;Residues: 1975-1991,2017-2039 <UM2>
A;Cross-references: UNIPARC:UPI0000174332; UNIPARC:UPI0000174333; GB:M27590
R;Sekiguchi, K.; Kloss, A.M.; Kurachi, K.; Yoshitake, S.; Hakomori, S.
Biochemistry 25, 4936-4941, 1986
A;Title: Human liver fibronectin complementary DNAs: identification of two different mes
A;Reference number: I52394; MUID:87026578; PMID:3021206
A;Accession: I65273
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1978-1990,2016-2018,'N',2020-2081,2113-2127 <SEK>
A;Cross-references: UNIPARC:UPI000006E04C; GB:M14060; NID:g182701; PIDN:AAAS2464.1; PID:
R;Kornblitt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
A;Title: Isolation and characterization of cDNA clones for human and bovine fibronectins
A;Reference number: A21165; MUID:83221567; PMID:6304699
A;Accession: A21165
A;Molecule type: mRNA
A;Residues: 2291-2386 <K03>
A;Cross-references: UNIPARC:UPI0000174334; GB:K00799; NID:g182681; PIDN:AAAS2460.1; PID:
R;Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 258, 12670-12674, 1983
A;Title: Primary structure of human plasma fibronectin.
A;Reference number: A92398; MUID:84032463; PMID:6630202
A;Accession: A92398
A;Molecule type: protein
A;Residues: 32-47,'C',49-51,'S',53-72,'A',74-290 <GAR1>
A;Cross-references: UNIPARC:UPI0000174335
R;Garcia-Pardo, A.; Gold, L.I.
Arch. Biochem. Biophys. 304, 181-188, 1993
A;Title: Further characterization of the binding of fibronectin to gelatin reveals the H
A;Reference number: S34791; MUID:93312001; PMID:8323285
A;Accession: S34791

A;Molecule type: protein
A;Residues: 291-300,551-560 <GAR2>
A;Cross-references: UNIPARC:UPI0000174336; UNIPARC:UPI0000174337
R;Griffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.
Thromb. Res. 43, 469-477, 1986
A;Title: Two plasma fibronectin fragments with different gelatin-binding properties.
A;Reference number: A60904; MUID:87019725; PMID:3532418
A;Accession: A60904
A;Molecule type: protein
A;Residues: 293-301 <GRI>
A;Cross-references: UNIPARC:UPI0000174338
R;Calaycay, J.; Pande, H.; Lee, T.; Borzi, L.; Siri, A.; Shively, J.E.; Zardi, L.
J. Biol. Chem. 260, 12136-12141, 1985
A;Title: Primary structure of a DNA- and heparin-binding domain (domain III) in human pla
A;Reference number: A23901; MUID:86008277; PMID:3900070
A;Accession: A23901
A;Molecule type: protein
A;Residues: 616-677,'Q',679-703,'PT', <CAL>
A;Cross-references: UNIPARC:UPI0000174339
R;Pierschbacher, M.D.; Ruoslahti, E.; Sundelin, J.; Lind, P.; Peterson, P.A.
J. Biol. Chem. 257, 9593-9597, 1982
A;Title: The cell attachment domain of fibronectin. Determination of the primary structur
A;Reference number: A92386; MUID:82265604; PMID:7050098
A;Accession: A92386
A;Molecule type: protein
A;Residues: 1441-1548 <PIE>
A;Cross-references: UNIPARC:UPI0000141CD5
A;Note: residues 1524-1527 are responsible for the cell-binding activity
R;Garcia-Pardo, A.; Rostagno, A.; Frangione, B.
Biochem. J. 241, 923-928, 1987
A;Title: Primary structure of human plasma fibronectin. Characterization of a 38 kDa dom
A;Reference number: A32517; MUID:87241275; PMID:3593230
A;Accession: A32517
A;Molecule type: protein
A;Residues: 1589-1630,'T',1722-2058 <GAR3>
A;Cross-references: UNIPARC:UPI000017433A
R;Tressel, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.E.; Pande
Biochem. J. 274, 731-738, 1991
A;Title: Human plasma fibronectin. Demonstration of structural differences between the A
A;Reference number: S14357; MUID:91190085; PMID:2012601
A;Accession: S14357
A;Molecule type: protein
A;Residues: 1614-1630,'T',1722-2081,2113-2244 <TRE>
A;Cross-references: UNIPARC:UPI000017433B
R;Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 260, 10320-10325, 1985
A;Title: Primary structure of human plasma fibronectin. Characterization of a 31,000-dalt
A;Reference number: A23891; MUID:85261459; PMID:4019516
A;Accession: A23891
A;Molecule type: protein
A;Residues: 2071-2080,2112-2356 <GAR4>
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C;Comment: The extra domain and connecting strand 3 are subject to developmental and tiss
C;Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins,
action, and transformation.
C;Genetics:
A;Gene: GDB.FN1
A;Cross-references: GDB:119135; OMIM:135600
A;Map position: 2q34-2q34
A;Introns: 49/3,1266/1,1357/1,1447/1,1487/1,1541/1,1631/1,1721/1,1991/1,2145/1
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C;Keywords: acute phase; alternative splicing; cell adhesion; collagen binding; duplicat
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F;141-179/Domain: fibronectin type I repeat homology <IF3>
F;186-225/Domain: fibronectin type I repeat homology <IF4>
F;231-270/Domain: fibronectin type I repeat homology <IF5>
F;308-608/Domain: collagen binding <CBR>
F;308-342/Domain: fibronectin type I repeat homology <IF6>

GenCore version 5.1.8
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(without alignments)
804.545 Million cell updates/sec

Title: US-09-581-651D-2
Perfect score: 3687
Sequence: 1 MLRGPGLLLAVQCLGTA.....ISKYLWRPVSIPPRNLGY 642

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3579.5	97.1	2386	1	US-09-016-366A-12
3	3578.5	97.1	2446	1	US-08-551-356-2
4	3578.5	97.1	2446	4	PCT-US93-12687-2
5	3439.5	93.3	2355	2	US-10-360-101-235
6	3433.5	93.1	2327	6	5455158-1
7	3422.5	92.8	2324	1	US-08-283-857-1
8	3422.5	92.8	2324	4	PCT-US95-09819-1
9	3406.5	92.4	2231	1	US-08-153-799-16
10	371	10.1	65	1	US-08-982-597A-19
11	371	10.1	65	2	US-09-136-218-19
12	298	8.1	663	2	US-09-194-468A-30
13	297	8.1	631	2	US-08-448-489-17
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16	297	8.1	660	2	US-09-521-220-18
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31	285.5	7.7	707	2	US-09-949-016-6575	Sequence 6575, Ap
32	285.5	7.7	708	2	US-08-448-489-16	Sequence 16, Appl
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35	278	7.5	48	1	US-08-982-597A-20	Sequence 20, Appl
36	278	7.5	48	1	US-09-136-218-20	Sequence 20, Appl
37	258	7.0	43	1	US-08-982-597A-21	Sequence 21, Appl
38	258	7.0	43	2	US-09-136-218-21	Sequence 21, Appl
39	220	6.0	96	1	US-08-717-169-2	Sequence 2, Appl
40	220	6.0	96	2	US-09-228-901A-2	Sequence 2, Appl
41	219.5	6.0	60	1	US-08-982-597A-18	Sequence 18, Appl
42	219.5	6.0	60	2	US-09-136-218-18	Sequence 18, Appl
43	208	5.6	1455	2	US-08-840-062-5	Sequence 5, Appl
44	206	5.6	37	1	US-08-982-597A-17	Sequence 17, Appl
45	206	5.6	37	2	US-09-136-218-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-09-961-403-1
; Sequence 1, Application US/09961403
; Patent No. 6780594
; GENERAL INFORMATION:
; APPLICANT: HE-STUMPP, HOLGER
; APPLICANT: HAENDLER, BERNARD
; APPLICANT: KRAETZSCHMAR, JOERN
; APPLICANT: KREFT, BERTHOLT
; APPLICANT: WINTERHAGER, ELKE
; APPLICANT: REGIDOR, PEDRO
; APPLICANT: SCOTTI, SIMONE
; TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
; FILE REFERENCE: SCH-1789
; CURRENT APPLICATION NUMBER: US/09/961,403
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2386
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-961-403-1

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RESULT 2
US-09-016-366A-12
; Sequence 12, Application US/09016366A
; Patent No. 5955431
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; APPLICANT: Huang, Chifu
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,366A
; FILING DATE: January 30, 1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,090
; FILING DATE: 05-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2386 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-366A-12

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RESULT 3
US-08-551-356-2
; Sequence 2, Application US/08551356
; Patent No. 5830700
; GENERAL INFORMATION:
; APPLICANT: Irani, Meher
; TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/551,356
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/349,762
; FILING DATE:
; APPLICATION NUMBER: US/07/998,271

GenCore version 5.1.8
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Title: US-09-581-651D-41

Perfect score: 54

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Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	54	100.0	642	8 ADS17489	Adsl17489 Amino aci
5	54	100.0	642	8 ADR97658	Adr97658 Human fib
6	54	100.0	642	9 ADW44480	Adw44480 Human fib
7	54	100.0	642	9 ADY55704	Ady55704 Human fib
8	54	100.0	642	9 ADY32458	Ady32458 Human fib
9	54	100.0	642	9 AEB56258	Aeb56258 Event seq
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12	54	100.0	657	9 ADZ26739	Adz26739 Human fib
13	54	100.0	660	2 AAY28901	Aay28901 Human mig
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15	38	70.4	145	4 ABB71381	Abb71381 Drosophil
16	38	70.4	279	7 ADF29037	Adf29037 M. globos
17	38	70.4	291	5 AAO15869	Aao15869 Talaromyc
18	38	70.4	291	5 AAO19509	Aao19509 T thermop
19	38	70.4	351	7 ABO79631	Abo79631 Pseudomon
20	38	70.4	500	4 AAU02826	Aau02826 Taxus cus
21	38	70.4	502	9 ADW72676	Adw72676 Taxus cus
22	37	68.5	40	6 ADA56768	Ada56768 Human sec
23	37	68.5	40	6 ADA40618	Ada40618 Human sec
24	37	68.5	40	7 ADB91474	Adb91474 Human sec

Query Match 100.0%; Score 54; DB 2; Length 20;

ALIGNMENTS

RESULT 1

AAY28902
ID AAY28902 standard; peptide; 20 AA.
XX
AC AAY28902;
XX
DT 21-SEP-1999 (first entry)
XX
DE MSF 1-alpha peptide epitope.
XX
KW Migration stimulatory factor; MSF; cell migration; modulation; human;
XX wound healing; scarring; MSF1-alpha; epitope; fibronectin.
XX Synthetic.
OS Homo sapiens.
XX
PN WO9931233-A1.
XX
PD 24-JUN-1999.
XX
PF 15-DEC-1998; 98WO-GB003766.
XX
PR 16-DEC-1997; 97GB-00026539.
XX
(UYDU-) UNIV DUNDEE.
XX
PI Schor SL, Schor AM;
XX
DR WPI; 1999-430039/36.
XX
PT Proteins with cell migration stimulatory activity used in treating wound
XX and preventing scarring.
XX
PS Claim 18; Page 57; 86pp; English.
XX
XX
CC The invention provides a human migration stimulatory factor (MSF)
CC protein. Host cells containing a replicable vector comprising the MSF
CC encoding nucleic acid can be used for the recombinant production of the
CC protein. The polypeptide can be used for modulating cell migration,
CC healing a wound and for preventing scarring. Sequences AAY28902-906
CC represent peptide epitopes of MSF against which monoclonal antibodies
CC that are specific to MSF and do not cross-react with fibronectin are
XX raised
XX
SQ Sequence 20 AA;

25 37 68.5 40 8 ADN41076 Adn41076 Novel hum
26 37 68.5 41 2 AAY02711 Aay02711 Human sec
27 37 68.5 41 7 ADA07390 Ada07390 Human sec
28 37 68.5 122 4 AAO06277 Aao06277 Human pol
29 37 68.5 362 7 ABM88358 Abm88358 Rice abio
30 37 68.5 485 4 AAU02835 Aau02835 Taxus cus
31 37 68.5 485 9 ADW72680 Adw72680 Taxus cus
32 37 68.5 515 8 ADN47628 Adn47628 Thermococ
33 37 68.5 3482 9 ADV24897 Adv24897 Anabaena
34 36 66.7 98 4 ABB16357 Abb16357 Human ner
35 36 66.7 150 4 ABG05775 Abg05775 Novel hum
36 36 66.7 154 3 AAB54331 Aab54331 Human pan
37 36 66.7 216 7 ADE61648 Ade61648 Rat Prote
38 36 66.7 243 5 ABP59149 Abp59149 Ribosomal
39 36 66.7 269 4 AAB92540 Aab92540 Human pro
40 36 66.7 281 5 ABB97335 Abb97335 Novel hum
41 36 66.7 291 2 AAR65437 Aar65437 Variant 1
42 36 66.7 294 8 ADR09348 Adr09348 Human pro
43 36 66.7 359 7 ABM88720 Abm88720 Rice abio
44 36 66.7 512 4 AAU02834 Aau02834 Taxus cus
45 36 66.7 578 4 ABG02192 Abg02192 Novel hum

Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; VSIPPRNLGY 10
| | | | | | | | | |
11 VSIPPRNLGY 20

QY 1 VSIPPRNLGY 10
| | | | | | | | | |
Db 633 VSIPPRNLGY 642

RESULT 2
ADQ39403
ID ADQ39403 standard; protein; 642 AA.
XX AC
XX ADQ39403;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human myocardial infarction-associated gene derived protein, SEQ ID 1066.
XX
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX
XX cardiant; gene therapy; human.
XX
XX Homo sapiens.
XX
XX WO2004058052-A2.
XX
XX 15-JUL-2004.
XX
XX 22-DEC-2003; 2003WO-US040978.
XX
XX 20-DEC-2002; 2002US-0434778P.
XX
XX 10-MAR-2003; 2003US-0453135P.
XX
XX 30-APR-2003; 2003US-0466412P.
XX
XX 23-SEP-2003; 2003US-0504955P.
XX
XX (APPL-) APPLERA CORP.
XX
XX Cargill M, Devlin JJ, Iakoubova O;
XX
XX WPI; 2004-533949/51.
XX
XX N-PSDB; ADQ38575.
XX
XX Identifying an individual who has an altered risk for developing
XX
XX myocardial infarction by detecting a single nucleotide polymorphism in
XX
XX the individual's nucleic acids.
XX
XX Claim 10; SEQ ID NO 1066; 145pp; English.
XX
XX The invention relates to a novel method for identifying an individual who
XX
XX has an altered risk for developing myocardial infarction. The method
XX
XX comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX
XX the nucleotide sequences given in the specification in the individual's
XX
XX nucleic acids, where the presence of the SNP is correlated with an
XX
XX altered risk for myocardial infarction in the individual. The invention
XX
XX further comprises: an isolated nucleic acid molecule comprising at least
XX
XX 8 contiguous nucleotides where one of the nucleotides is an SNP given in
XX
XX the specification or its complement and encoding any one of the amino
XX
XX acid sequences given in the specification; an isolated polypeptide
XX
XX comprising an amino acid sequence given in the specification; an antibody
XX
XX that specifically binds to the polypeptide or its antigen-binding
XX
XX fragment; an amplified polynucleotide containing an SNP given in the
XX
XX specification and which is between about 16 and 1000 nucleotides in
XX
XX length; a kit for detecting an SNP in a nucleic acid, comprising the
XX
XX polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
XX
XX nucleic acid molecule; a method of detecting a variant polypeptide; and a
XX
XX method for identifying an agent useful in treating or preventing
XX
XX myocardial infarction. The novel detection method has cardiant activity.
XX
XX The nucleic acids of the invention may be used in gene therapy. The
XX
XX method is useful in identifying an individual who has an increased or
XX
XX decreased risk for developing myocardial infarction and for preparing a
XX
XX composition for treating or preventing myocardial infarction. This
XX
XX sequence represents the protein of a human myocardial infarction.
XX
XX associated gene containing one or more SNP's of the invention. Note: This
XX
XX sequence was not shown in the specification. The sequence has come from

CC an electronic sequence listing downloaded from the WIPO website.
XX
XX
SQ Sequence 642 AA;
Query Match 100.0%; Score 54; DB 8; Length 642;
Best Local Similarity 100.0%; Pred. No. 0.51; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; VSIPPRNLGY 10
| | | | | | | | | |
Db 633 VSIPPRNLGY 642

RESULT 3
ADR67316
ID ADR67316 standard; protein; 642 AA.
XX AC
XX ADR67316;
XX
XX 02-DEC-2004 (first entry)
XX
XX Human bladder cancer associated amino acid sequence.
XX
XX bladder cancer tissue; bladder cancer; cytostatic.
XX
XX Homo sapiens.
XX
XX WO2004076613-A2.
XX
XX 10-SEP-2004.
XX
XX 24-FEB-2004; 2004WO-DE000364.
XX
XX 26-FEB-2003; 2003DE-01009729.
XX
XX (HERR/) HERR A.
XX
XX (HINZ/) HINZMANN B.
XX
XX (DAHL/) DAHL E.
XX
XX (STAU/) STAU E.
XX
XX (PILA/) PILARSKY C.
XX
XX (SPEC/) SPECHT T.
XX
XX Herr A, Hinzmann B, Dahl E, Staub E, Pilarsky C, Specht T;
XX
XX WPI; 2004-653385/53.
XX
XX New nucleic acids, and encoded proteins, from bladder cancer tissue,
XX
XX useful for diagnosis, treatment and in screening for specific binding
XX
XX agents.
XX
XX Claim 2; Fig 3; 112pp; German.
XX
XX The present invention describes nucleic acids (I) associated with bladder
XX
XX cancer tissue. Also described: (1) peptides and proteins (II) containing
XX
XX an amino acid sequence encoded by (I); (2) a method for diagnosing
XX
XX bladder cancer (BC) or monitoring its progression, that uses (I); (II)
XX
XX or agents (Z) that inhibit, or bind to, (I) or (II), labelled with a
XX
XX reporter; and (3) a method for treating BC that uses (I), (II) or (Z).
XX
XX (I) and (II) have cytostatic activity. (I) and (II) can be used to detect
XX
XX (and monitor progression of) bladder cancer (BC), or the risk of
XX
XX developing it; to screen for specific binding agents (Z), and to treat
XX
XX BC. (Z) are also useful as diagnostic and therapeutic agents. The present
XX
XX sequence represents a human amino acid sequence associated with bladder
XX
XX cancer, which is used in the exemplification of the present invention.
XX
XX
SQ Sequence 642 AA;
Query Match 100.0%; Score 54; DB 8; Length 642;
Best Local Similarity 100.0%; Pred. No. 0.51; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; VSIPPRNLGY 10
| | | | | | | | | |
QY 1 VSIPPRNLGY 10
| | | | | | | | | |


```
Db      633 VSIPPRNLGY 642

RESULT 4
ADS17489
ID      ADS17489 standard; protein; 642 AA.
XX
XX
AC      ADS17489;
XX
XX
DT      02-DEC-2004 (first entry)
XX
XX
DE      Amino acid sequence of human fibronectin 1.
XX
XX
KW      cell state; time-lapse profile; protein-protein interaction;
KW      drug screening; cancer; infectious disease; allergy; hypertension;
KW      hyperlipaemia; diabetes; cardiac disease; cerebral infarction; dementia;
KW      obesity; arteriosclerosis; infertility; mental disease; nervous disease;
KW      cataract; progeria; hypersensitivity; ultraviolet radiation; human;
KW      fibronectin 1; actin acting substance; transfection array.
XX
XX
OS      Homo sapiens.
XX
XX
WO2004079007-A2.
XX
XX
PD      16-SEP-2004.
XX
XX
PF      03-MAR-2004; 2004WO-JP002694.
XX
XX
PR      04-MAR-2003; 2003JP-00057870.
XX
XX
PA      (NAAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
PI      Miyake M, Yoshikawa T, Uchimura E, Miyake J;
XX
XX
WPI; 2004-662438/64.
XX
XX
DR      N-PSDB; ADS17488.
XX
XX
PT      Presenting a state of a cell, useful for diagnosing and treating a
PT      disease, e.g. cancer, infectious disease, allergy, diabetes, dementia,
PT      obesity, infertility, or cataract, comprises obtaining a time-lapse
PT      profile of the cell.
XX
XX
PS      Disclosure; SEQ ID NO 2; 532pp; English.
XX
XX
CC      The specification describes a method and system for accurately presenting
CC      a state of a cell. The method comprises obtaining a time-lapse profile of
CC      the cell by time-lapse monitoring of a gene state associated with at
CC      least one gene derived from the cell, and presenting the time-lapse
CC      profile. The gene comprises a transcription control sequence, and the
CC      gene state includes expression of the gene. The method and system are
CC      useful presenting a state of a cell. The method can allow the elucidation
CC      of key protein-protein interactions suitable for targeting by drug
CC      screening protocols. The method is useful for diagnosing or treating a
CC      disease, e.g. cancer, infectious disease due to viruses or bacteria,
CC      allergy, hypertension, hyperlipaemia, diabetes, cardiac disease, cerebral
CC      infarction, dementia, obesity, arteriosclerosis, infertility, mental and
CC      nervous diseases, cataract, progeria, or hypersensitivity to ultraviolet
CC      radiation. The present sequence represents human fibronectin 1. Bovine
CC      fibronectin was used as a candidate for an actin acting substance. The
CC      actin acting substance was used with transfection reagents and amplified
CC      plasmid DNA in assays using transfection arrays, in the course of the
CC      invention.
XX
XX
SQ      Sequence 642 AA;

Query Match      100.0%; Score 54; DB 8; Length 642;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 VSIPPRNLGY 10
        |||||
Db      633 VSIPPRNLGY 642

RESULT 6
ADW44480
ID      ADW44480 standard; protein; 642 AA.
XX
XX
AC      ADW44480;
XX
XX
DT      24-MAR-2005 (first entry)
XX
XX
```

Composition comprising an actin acting substance or an actin acting substance and a target substance, useful for increasing the efficiency of introducing a target substance into a cell and in cell biology or genetic engineering.

Claim 4; SEQ ID NO 2; 347pp; English.

This invention relates to a novel composition and method for increasing the efficiency of introducing a target substance into a cell. Specifically, it refers to the introduction of DNA (e.g. the gene of interest to be transfected), polypeptides, sugars or complexes thereof into a cell, and comprises an actin acting substance. The present invention describes the actin acting substance as an extracellular matrix protein, a variant or fragment thereof selected from fibronectin, laminin or vitronectin. The composition further comprises a gene introduction reagent selected from cationic polymers, cationic lipids, and calcium phosphate, as well as a gold colloid particle that is contacted with the cell. As such, the composition, kit, device or method is useful for increasing the efficiency of introducing a target substance into a cell and thus is useful in the fields of cell biology, genetic engineering and molecular biology. This polypeptide sequence is the human fibronectin protein sequence of the invention.

Sequence 642 AA;

Query Match 100.0%; Score 54; DB 8; Length 642;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VSIPPRNLGY 10
|||
Db 633 VSIPPRNLGY 642

RESULT 6
ADW44480
ID ADW44480 standard; protein; 642 AA.
XX
XX
AC ADW44480;
XX
XX
DT 24-MAR-2005 (first entry)
XX
XX

DE Human fibronectin 1.
XX cell transduction; nerves; cell adhesion; fibronectin 1.
XX Homo sapiens.
OS
XX WO2005001090-A1.
XX 06-JAN-2005.
XX
XX 25-JUN-2004; 2004WO-JP009568.
XX
XX 26-JUN-2003; 2003JP-00183630.
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX Miyake M, Uchimura E, Yoshikawa T, Miyake J;
XX WPI; 2005-091515/10.
XX N-PSDB; ADW44479.
XX Composition useful for improving transduction efficiency of nucleic acid
XX into cell, comprises cell adhesion molecule and gene-transfer reagent.
XX
XX Disclosure; SEQ ID NO 24; 446pp; Japanese.
XX
XX This invention describes a novel composition for improving transduction
XX efficiency of a nucleic acid into a cell from nervous tissue which
XX comprises a cell adhesion molecule and a gene-transfer reagent. The
XX invention also describes a device, kit and novel method for improving
XX nucleic acid transduction efficiency of a cell on a solid phase. The cell
XX adhesion molecule contains an extracellular matrix chosen from collagen,
XX laminin and fibronectin. The gene transfer reagent comprises a cationic,
XX polymer, cationic liquid, polyanine type reagent, polyanine type reagent
XX or calcium phosphate. This sequence represents human fibronectin 1, which
XX is used in the composition of the invention.
XX
XX Sequence 642 AA;
SQ
Query Match 100.0%; Score 54; DB 9; Length 642;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSIPPRNLGY 10
Db 633 VSIPPRNLGY 642
RESULT 7
ADY55704
ID ADY55704 standard; protein; 642 AA.
XX
XX ADY55704;
XX
XX 19-MAY-2005 (first entry)
XX Human fibronectin 1 protein.
XX
XX biocomputer; drug screening; diagnosis; food; cosmetics; agriculture;
XX analysis; fibronectin.
XX
XX Homo sapiens.
XX
XX WO2005021744-A1.
XX
XX 10-MAR-2005.
XX
XX 25-JUN-2004; 2004WO-JP009404.
XX
XX 25-JUN-2003; 2003JP-00181915.
XX 07-AUG-2003; 2003JP-00289469.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA

XX Miyake M, Yoshikawa T, Miyake J;
XX WPI; 2005-262218/27.
XX N-PSDB; ADY55703.
XX
XX Performing data production and presenting cell information under a
XX similar environment as digital cells, useful e.g. in drug development,
XX comprises profiling the actual status of cells.
XX
XX Example 14; SEQ ID NO 2; 517pp; Japanese.
XX
XX The invention relates to a novel method for producing profile data that
XX relates to cell information in an identical environment. The method
XX comprises placing several cells on a support in the same environment, and
XX monitoring the biological factors on or in the cells or their aggregate
XX chronologically to generate profile data of the cells. The methods and
XX systems are useful for performing data production by profiling actual
XX status of cells, and for presenting time-lapse and/or real-time cell
XX information at a cellular level under a similar environment as well as
XX digital cells in the form of a library of databases with cell
XX information, which are particularly useful in drug development, disease
XX diagnosis and management, as well as in fields including food technology,
XX cosmetics, agriculture, environmental sciences, in silico computational
XX biological studies, cell analysis and biotechnology. The methods and
XX systems are capable of providing information with controllability, This
XX specificity and most importantly directly even in complex systems. This
XX sequence represents a human fibronectin 1 protein used in the method for
XX producing a digital cell profile of the invention.
XX
XX Sequence 642 AA;
SQ
Query Match 100.0%; Score 54; DB 9; Length 642;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSIPPRNLGY 10
Db 633 VSIPPRNLGY 642
RESULT 8
ADY32458
ID ADY32458 standard; protein; 642 AA.
XX
XX ADY32458;
XX
XX 19-MAY-2005 (first entry)
XX Human fibronectin protein.
XX
XX biochip; fluorescence; fibronectin.
XX
XX Homo sapiens.
XX
XX JP2005052050-A.
XX
XX 03-MAR-2005.
XX
XX 01-AUG-2003; 2003JP-00285471.
XX
XX 01-AUG-2003; 2003JP-00285471.
XX (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
XX
XX WPI; 2005-199806/21.
XX N-PSDB; ADY32457.
XX
XX Disc-like biochip useful for printing biomolecules such as DNA, comprises
XX cell fixed to disc-like solid phase support body.
XX
XX Claim 16; SEQ ID NO 2; 43pp; Japanese.
XX

CC The invention relates to a novel disc-like biochip, comprising a cell
 CC fixed to a disc-like solid phase support body. The invention further
 CC comprises: a reader of the disc-like biochip in order to read the spot on
 CC the chip and a detection unit to detect the signal produced from the
 CC spot. The disc-like biochip is useful for printing biomolecules such as
 CC DNA at high speed. The reader of the biochip performs fluorescent reading
 CC in a cheap and simple manner. This sequence represents a human
 CC fibronectin protein used in the novel biochip detection device of the
 CC invention.

XX
 XX SQ Sequence 642 AA;

Query Match 100.0%; Score 54; DB 9; Length 642;
 Best Local Similarity 100.0%; Pred. No. 0.51;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSIPPRNLGY 10
 DB 633 VSIPPRNLGY 642
 |||||

RESULT 9
 AEB56258
 ID AEB56258 standard; protein; 642 AA.
 XX
 AC AEB56258;
 XX
 DT 20-OCT-2005 (first entry)
 XX
 DE Event sequencer related protein SEQ ID NO 2.
 XX
 DE analyte detection.
 XX
 OS Unidentified.
 XX
 OS
 XX PN W02005073890-A1.
 XX
 PD 11-AUG-2005.
 XX
 XX 27-JAN-2005; 2005WO-JP001151.
 XX
 PF 30-JAN-2004; 2004JP-00024923.
 XX
 PR (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 XX
 PI Miyake M, Yoshikawa T, Miyake J;
 XX
 DR WPI; 2005-571425/58.
 DR N-PSDB; AEB56257.
 XX
 XX Event sequencer extracts portion of timer series data with peculiar
 PT behavior associated with index of system, as event timing, to generate
 PT event descriptor described by event timing.
 XX
 XX Disclosure; SEQ ID NO 2; 281pp; Japanese.

XX
 CC The invention relates to an event sequencer that acquires time-series
 CC data on an index derived from a system and provides a peculiar behavior
 CC associated with the index. A portion of time series data having the
 CC peculiar behavior is extracted as an event timing and an event descriptor
 CC described by the event timing is generated. The sequencer is useful for
 CC analysis of the state of a system. The sequencer performs meaningful
 CC analysis of a system state using specific index effectively. The present
 CC sequence represents the amino acid sequence of an event sequencer related
 CC protein.

XX
 XX SQ Sequence 642 AA;

Query Match 100.0%; Score 54; DB 9; Length 642;
 Best Local Similarity 100.0%; Pred. No. 0.51;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSIPPRNLGY 10

Db |||||
 633 VSIPPRNLGY 642

RESULT 10
 AEB78062

ID AEB78062 standard; protein; 642 AA.

XX
 AC AEB78062;

XX
 DT 20-OCT-2005 (first entry)

XX
 DE Human fibronectin 1.

XX
 KW Transfection; fibronectin; cell adhesion; gene transfer.

XX
 OS Homo sapiens.

XX
 PN W02005073385-A1.

XX
 PD 11-AUG-2005.

XX
 PF 27-JAN-2005; 2005WO-JP001148.

XX
 PR 29-JAN-2004; 2004JP-00022315.

XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX
 PI Miyake M, Yoshikawa T, Uchimura E, Miyake J;

XX
 DR WPI; 2005-555702/56.

DR
 N-PSDB; AEB78061.

XX
 PT Composition for elevating transfer efficiency of target substance into
 PT cells, comprises cell adhesion-related factor.

XX
 PS Disclosure; SEQ ID NO 2; 101pp; Japanese.

XX
 CC The invention relates to a composition (I) for elevating the transfer
 CC efficiency of a target substance into cells, comprises a cell adhesion-
 CC related factor. Also included are a kit (K1) for elevating gene transfer
 CC efficiency comprising cell-adhesion related factor, and a gene transfer
 CC reagent), a composition (II) for introducing a target substance into a
 CC cell (comprising a target substance, and a cell-adhesion related factor),
 CC a device (III) for elevating transfer efficiency of target substance into
 CC cell (comprising a target substance and a cell-adhesion related factor,
 CC where the cell-adhesion related factor was immobilized to a support) and
 CC elevating (M1) the transfer efficiency of a target substance into cells
 CC (involving providing a target substance and a cell-adhesion related
 CC factor, and contacting the target substance and the cell-adhesion related
 CC factor with the cell). The cell-adhesion related factor contains an
 CC interaction substance capable of interacting with cell adhesion molecule
 CC (e.g. the extracellular matrix). The cell adhesion molecule contains
 CC integrin receptor or RGD motif. The interaction substance carries out an
 CC antigen antibody reaction to partner of the cell adhesion molecule. The
 CC interaction substance is an antibody or its derivative(s). The
 CC interaction substance contains an antibody chosen from anti-CD49a
 CC antibody, anti-CD49b antibody, anti-CD49c antibody, anti-CD49e antibody
 CC and anti-CD49f antibody. The integrin receptor is chosen from CD49a,
 CC CD49b, CD49c, CD49d, CD49e, CD49f and CD29. The integrin receptor interacts with
 CC CD49c, CD49d, CD49e, CD49f and CD29. The integrin receptor interacts with
 CC molecule chosen from collagen, fibronectin, vitronectin and laminin. (I),
 CC (K1), (II) or (M1) are useful for elevating the transfer efficiency of a
 CC target substance into cells, where the target substance is a genetic
 CC material (nucleic acid molecule), preferably DNA, and the cell is at
 CC least one cell chosen from stem cell and differentiation cell. (II) is
 CC useful for introducing a target substance into a cell, where the target
 CC substance is chosen from DNA, RNA, polypeptide, saccharide, and their
 CC complex, preferably DNA. (I) enables to improve the transfer efficiency
 CC under any conditions (solid or liquid phase) in the case of transferring
 CC a target substance that can be hardly transferred into cells. The present
 CC sequence represents human fibronectin 1. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 642 AA;

Query Match 100.0%; Score 54; DB 9; Length 642;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSIPPRNLGY 10
Db 633 VSIPPRNLGY 642
|||||

RESULT 11
ADQ39409
ID ADQ39409 standard; protein; 657 AA.
XX
AC ADQ39409;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1072.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Takoubova O;
DR WPI; 2004-533949/51.
DR N-PSDB; ADQ38581.
XX

Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1072; 145pp; English.
XX

The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The

CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 657 AA;

Query Match 100.0%; Score 54; DB 8; Length 657;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSIPPRNLGY 10
Db 648 VSIPPRNLGY 657
|||||

RESULT 12
AD226739
ID AD226739 standard; protein; 657 AA.
XX
AC AD226739;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human fibronectin.
XX
KW cell culture; stem cell; fibronectin.
XX
OS Homo sapiens.
XX
PN WO2005030999-A1.
XX
PD 07-APR-2005.
XX
PF 24-SEP-2004; 2004WO-US031524.
XX
PR 25-SEP-2003; 2003US-0506221P.
PR 08-OCT-2003; 2003US-0509594P.
XX
PA (DAND) DANA FARBER CANCER INST INC.
XX
PI Ritz J, Wu CJ;
XX
DR WPI; 2005-273394/28.
DR N-PSDB; AD226738.
XX

Detecting lineage-specific cells in a biological sample, useful for
PT determining the clinical outcome of a progenitor cell transfer in a
PT subject, comprises identifying lineage-specific mRNA in the sample.
XX
PS Disclosure; SEQ ID NO 365; 393pp; English.
XX

The invention relates to a method of detecting lineage-specific cells in
CC a biological sample which comprises identifying lineage-specific mRNA in
CC the sample. The methods are useful for determining the clinical outcome
CC of a progenitor cell transfer in a subject, and for identifying or
CC quantifying lineage-specific cells. The present sequence represents the
CC amino acid sequence of a human protein used to identify lineage-specific
CC cells.
XX
SQ Sequence 657 AA;

Query Match 100.0%; Score 54; DB 9; Length 657;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSIPPRNLGY 10
Db 648 VSIPPRNLGY 657
|||||

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RESULT 13
AA28901
ID AAY28901 standard; protein; 660 AA.
XX
XX AC AAY28901;
XX
XX 21-SEP-1999 (first entry)
XX
XX Human migration stimulating factor (MSF) 1-alpha protein.
XX
XX Migration stimulatory factor; MSF; cell migration; modulation; human;
XX wound healing; scarring; MSF1-alpha.
XX
XX Homo sapiens.
XX
XX WO991233-A1.
XX
XX 24-JUN-1999.
XX
XX 15-DEC-1998; 98WO-GB003766.
XX
XX 16-DEC-1997; 97GB-00026539.
XX
XX (UYDU-) UNIV DUNDEE.
XX
XX Schor SL, Schor AM;
XX
XX WPI; 1999-430039/36.
XX
XX N-PSDB; AAX81299.
XX
XX Proteins with cell migration stimulatory activity used in treating wound
XX and preventing scarring.
XX
XX Claim 1; Page 53; 86pp; English.
XX
XX The invention provides a human migration stimulatory factor (MSF)
XX protein. Host cells containing a replicable vector comprising the MSF
XX encoding nucleic acid can be used for the recombinant production of the
XX protein. The polypeptide can be used for modulating cell migration,
XX healing a wound and for preventing scarring. The present sequence
XX represents the human MSF1-alpha protein
XX
XX Sequence 660 AA;
XX
XX Query Match 100.0%; Score 54; DB 2; Length 660;
XX Best Local Similarity 100.0%; Pred. No. 0.53;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 VSIPPRNLGY 10
DB 651 VSIPPRNLGY 660
|||||
|

RESULT 14
AA65443
ID AAR65443 standard; protein; 291 AA.
XX
XX AAR65443;
XX
XX 25-MAR-2003 (revised)
XX
XX 17-JUL-1995 (first entry)
XX
XX Variant lipase D96W+E210N, used in detergent compositions.
XX
XX lipase; variant; catalytic triad; lipid contact zone; active Serine;
XX wash performance; detergent; dishwashing; softening composition.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Protein 23..291
XX /label= mature_lipase

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FT Region 43..47
FT /note= "lipid contact zone"
FT Region 48..50
FT /note= "lipid contact zone"
FT Region 78..84
FT /note= "lipid contact zone"
FT Region 103..120
FT /note= "lipid contact zone"
FT Misc-difference 118
FT /label= D96W
FT Region 132..138
FT /note= "lipid contact zone"
FT Region 166..169
FT /note= "lipid contact zone"
FT Region 194..198
FT /note= "lipid contact zone"
FT Region 221..235
FT /note= "lipid contact zone"
FT Misc-difference 232
FT /label= E210N
FT Region 270..291
FT /note= "lipid contact zone"
XX WO9425577-A1.
XX
XX 10-NOV-1994.
XX
XX 22-APR-1994; 94WO-DK000162.
XX
XX 23-APR-1993; 93DK-00000466.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Svendsen A, Patkar SA, Gormsen E, Clausen IG;
XX WPI; 1994-358256/44.
XX
XX New lipase variant with non-aromatic amino acid replaced - in the lipid
XX contact zone, and related DNA, vectors and transformed cells, useful in
XX detergent compens. etc.
XX
XX Claim 6; Page 32-34; 44pp; English.
XX
XX This polypeptide is a variant of the Humicola lanuginosa lipase shown in
XX AAR65394. This variant contains a double mutation, where at position 96,
XX the wild type aspartic acid is substituted with tryptophan and at
XX position 210, the wild type glutamic acid is substituted with asparagine.
XX Variants are constructed in which a non-aromatic amino acid in the lipid
XX contact zone is replaced with an aromatic amino acid (see also AAR65396-
XX 442 and AAR65444-449). The parent lipase has a trypsin-like catalytic
XX triad including an active serine in a hydrophobic, elongated binding
XX pocket in the lipid contact zone (located in the part of the lipase
XX structure contg. the active Ser and involved in interaction with the
XX substrate at or during hydrolysis). Some variants were constructed in
XX which one or more amino acid residues were replaced in specific positions.
XX The variants are useful as additives for detergent, dishwashing and
XX softening compens. They provide better wash performance (with
XX improvement factors as high as 4) than wild type enzymes. (Updated on 25-
XX MAR-2003 to correct PN field.)
XX
XX Sequence 291 AA;
XX
XX Query Match 74.1%; Score 40; DB 2; Length 291;
XX Best Local Similarity 75.0%; Pred. No. 78;
XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
QY 3 IPPRNLGY 10
DB 228 LPPRNFY 235
|||||
|

RESULT 15
ABB71381

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ID ABB71381 standard; protein; 145 AA.
XX AC ABB71381;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 40935.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX OS pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX N-PSDB; ABL15484.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX PS Disclosure; SEQ ID NO 40935; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 145 AA;

Query Match 70.4%; Score 38; DB 4; Length 145;
Best Local Similarity 77.8%; Pred. No. 86;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VSIPPPNLG 9
Db 81 VSIPPPNMG 89

Search completed: May 10, 2006, 19:20:06
Job time : 10.4356 secs